

David Schreber SEARCH REQUEST FORM

Access DB# 171080

Scientific and Technical Information Center

CRFE

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 3/9
Unit: 1635 Phone Number: 2-0765 Serial Number: 09/699-667
Mail Box and Bldg/Room Location: 2-D-28 Results Format Preferred (circle): PAPER DISK E-MAIL
LC18

more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.
Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or
ity of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if
own. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of invention: MA enzyme w/
inventors (please provide full names): Perreault

Articles: Priority Filing Date: 10/30/00
For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the
appropriate serial number.

5-Ma-37 Please Search Seq ID Nos. 65, 66,
67Ma-20
3-Ma-37 63, 64 + 61 + 62
4-Ma-20 (See attached
1-Ma-57 claims 20-23)
2-Ma-57 NO interference please.

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STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher: <u>P. Schreber</u>	NA Sequence (#) <u>12</u>	STN	
Searcher Phone #: <u>272-2526</u>	AA Sequence (#)	Dialog	
Searcher Location: <u>Remsh E01A6</u>	Structure (#)	Questel/Orbit	
Date Searcher Picked Up:	Bibliographic	Dr. Link	
Date Completed: <u>3/18</u>	Litigation	Lexis/Nexis	
Searcher Prep. Review Time <u>16</u>	Fulltext	Sequence Systems: <u>CompuGen</u>	
Clerical Prep. Time:	Patent Family	WWW/Internet	
Outline Time <u>9</u>	Other	Other (specify)	

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Result No.	Score	Query #		Length	DB	ID	Description
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2	35.4	95.7	57	6	AX012282	Sequence	
3	35.4	95.7	57	6	AX012283	Sequence	
4	35.4	95.7	57	6	AX012284	Sequence	
5	35.4	95.7	57	6	AX012285	Sequence	
6	35.4	95.7	57	6	AX012286	Sequence	
7	35.4	95.7	57	6	AX012287	Sequence	
8	35.4	95.7	57	6	AX012288	Sequence	
9	35.4	95.7	57	6	AX012289	Sequence	
10	35.4	95.7	57	6	AX012290	Sequence	
11	30	81.1	52	6	AX012290	Sequence	
12	30	81.1	52	6	AR021007	Sequence	
13	30	81.1	52	6	AR021047	Sequence	
14	30	81.1	52	6	AR043422	Sequence	
15	30	81.1	52	6	AR043462	Sequence	
16	30	81.1	52	6	AR062337	Sequence	
17	30	81.1	52	6	AR062377	Sequence	
18	30	81.1	52	6	AR183796	Sequence	
19	30	81.1	52	6	AR183836	Sequence	
20	30	81.1	52	6	AR1368179	Sequence	

RESULT 2	AX012282	AX012282	Sequence 44 from Patent WO9955856.	57 bp	RNA	linear	PAT 06-SEP-2000
LOCUS	AX012282						
DEFINITION	AX012282						
ACCESSION	AX012282						
VERSION	AX012282.1		GI:9998343				
KEYWORDS	.						
SOURCE		synthetic construct					
ORGANISM		synthetic construct					

```
other sequences; artificial sequences.
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
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Best Local Similarity 59.5%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGTCCACCTCTCGCGGTCCGACCTGGGCATGCGC 37
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RESULT 3
AX012283
LOCUS AX012283 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 45 from Patent WO9955856.
ACCESSION AX012283
VERSION AX012283.1 GI:9998344
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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source Location/Qualifiers
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Best Local Similarity 59.5%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
AX012284
LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"
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Best Local Similarity 59.5%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCGCGGNNNNNGGCAUGCBSY 37
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AX012285
LOCUS AX012285 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 47 from Patent WO9955856.
ACCESSION AX012285
VERSION AX012285.1 GI:9998346
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GGGTCCACCTCTCGCGGTCCGACCTGGGCATGCGC 37
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RESULT 6
AX012286
LOCUS AX012286 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 48 from Patent WO9955856.
ACCESSION AX012286
VERSION AX012286.1 GI:9998347
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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AR021007 LOCUS AR021007 52 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 40 from patent US 5789245.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 11:20:37 ; Search time 205.285 Seconds
(without alignments)
1066.957 Million cell updates/sec

Title: US-09-699-667E-65
Perfect score: 37
Sequence: 1 ggguccacucccggunnnnnnggcaugcaby 37

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4316768

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35.4	95.7	37	AAZ57639	Aaz57639 Nucleotid
2	35.4	95.7	57	AAZ57636	Aaz57636 Trans-act
3	35.4	95.7	57	AAZ57638	Aaz57638 Trans-act
4	35.4	95.7	57	AAZ57637	Aaz57637 Trans-act
5	30	81.1	48	ADR47040	Adi-47040 Dengue vi
6	30	81.1	48	ADT48965	Adt-48965 PCR prime
7	30	81.1	51	AAQ86173	Aaq86173 Primer HD
8	30	81.1	52	AAQ86204	Aaq86204 Sindbis/H
9	30	81.1	52	AAT31151	Aat31151 HDV rever
10	30	81.1	52	AAT30817	Aat30817 HDV riboz
11	30	81.1	52	AAV42394	Aav42394 Nested PC
12	30	81.1	52	AAV42426	Aav42426 Forward P
13	30	81.1	52	AAV60154	Aav60154 Nested PC
14	30	81.1	52	AAV60185	Aav60185 Reverse P
15	30	81.1	52	AAV70746	Aav70746 Reverse P
16	30	81.1	52	AAV70714	Aav70714 Nested pr
17	30	81.1	52	AAZ92930	Aaz92930 Hepatitis
18	30	81.1	52	AAZ92970	Aaz92970 Hepatitis
19	30	81.1	52	AAZ92843	Aaz92843 Hepatitis
20	30	81.1	52	AAZ92803	Aaz92803 Hepatitis

21	30	81.1	52	6	AAZ38850	Aal38850 Alphaviru
22	30	81.1	52	6	AAZ38810	Aal38810 Alphaviru
23	30	81.1	52	6	ABK46276	Abk46276 HDV anti
24	30	81.1	52	6	ABK46316	Abk46316 Hepatitis
25	30	81.1	52	12	ADI30383	Adi30383 Hepatitis
26	30	81.1	52	12	ADI30423	Adi30423 Hepatitis
27	30	81.1	52	12	ADO13982	Ado13982 Eukaryoti
28	30	81.1	52	12	ADO13942	Ado13942 Eukaryoti
29	30	81.1	57	12	ADH10551	Adh10551 Hepatitis
30	29	78.4	56	2	AAZ59264	Aaz59264 Nested pr
31	29	78.4	56	2	AAZ58506	Aaz58506 Nested pr
32	29	78.4	56	8	ABX81463	Abx81463 Sindbis v
33	29	78.4	56	9	ADA50686	Ada50686 Sindbis v
34	28	75.7	45	2	AAZ78132	Aaz78132 Hepatitis
35	27	73.0	49	2	AAV61451	Aav61451 Hepatitis
36	27	73.0	49	2	AAZ63356	Aaz63356 Human Hep
37	27	73.0	49	2	AAV72941	Aav72941 Human Hep
38	27	73.0	49	2	AAZ00071	Aaz00071 Human Hep
39	27	73.0	49	2	AAV81895	Aav81895 Human Hep
40	27	73.0	49	2	AAV93887	Aav93887 Human Hep
41	24	64.9	52	2	AAQ46668	Aaq46668 Substrate
42	23.4	63.2	57	12	ADP69915	Adp69915 LacZnl812
43	23	62.2	58	2	AAT38753	Aat38753 Primer us
44	23	62.2	58	5	AAZ28149	Aaz28149 Primer #3
45	22.6	61.1	35	2	AAT37961	Aat37961 Ribozyme

ALIGNMENTS

RESULT 1	AAZ57639	standard; RNA; 37 BP.
ID	AAZ57639	
XX	AAZ57639;	
AC	AAZ57639;	
XX	05-APR-2000	(first entry)
DT	05-APR-2000	(first entry)
XX	Nucleotide sequence of bimolecular ribozyme Rza fragment.	
DE	Nucleotide sequence of bimolecular ribozyme Rza fragment.	
XX	Bimolecular ribozyme; viral RNA cleavage; Rza fragment;	
KW	Bimolecular ribozyme; viral RNA cleavage; Rza fragment;	
XX	inherited disease; ss.	
OS	Synthetic.	
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EH	Key	1..6
FT	misc_binding	/tag= a
FT		/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT		/note= "Forms double-stranded region with bases 20-16 of sequence AAZ57640"
FT	stem_loop	7..19
FT		/tag= b
FT	misc_binding	20..25
FT		/tag= c
FT		/bound_moiety= "Ribozyme substrate Pl.1"
FT		/note= "Forms double-stranded region with bases 11-6 of sequence AAZ57641"
FT	misc_binding	30..37
FT		/tag= d
FT		/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT		/note= "Forms double-stranded region with bases 8-1 of sequence AAZ57640"
XX	WO9955856-A2.	
XX	04-NOV-1999.	
PD	04-NOV-1999.	
XX	29-APR-1999;	99WO-CA0000391.
PF	29-APR-1999;	98CA-02230203.
XX	29-APR-1998;	
PR	29-APR-1998;	
XX	(UYSH) UNIV SHERBROOKE.	
PA		


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PR 29-APR-1998; 98CA-02230203.
XX
PA (UYSH ) UNIV SHERBROOKE.
XX
PI Perreault J, Ananvoranich S, Lafontaine D;
XX
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
PS Example 1; Fig 2; 52pp; English.
XX
CC This is the nucleotide sequence of a trans-acting antigenomic delta
CC ribozyme of the invention. This ribozyme cleaves substrate SPI.1 (see
CC AAZ57641). The invention relates to a nucleic acid enzyme (e.g.
CC deltaRzPl.1) that is constructed to have a substrate binding portion with
CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
CC sequence 5'-H'-GNHHNN-3'. The binding portion of the enzyme (ribozyme)
CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
CC (cleavage site is represented by *). At least one nucleotide is present
CC 5' to the cleavage site of the substrate sequence. The enzyme of the
CC invention is used to cleave a substrate nucleotide sequence at a specific
CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
CC to cleave viral RNA or RNA causing for example an inherited disease. The
CC enzymes also have other therapeutic, biotechnological and diagnostic
CC applications. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match 95.7%; Score 35.4; DB 3; Length 57;
Best Local Similarity 73.0%; Pred. No. 0.42;
Matches 27; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCUCCGCGGUNNNNNNGGCAUGCBSY 37
Db 1 GGGUCCACCUCUCCGCGGCGGCCGACCGUCCGCAUGCCUU 37

RESULT 4
AAZ57637
ID AAZ57637 standard; RNA; 57 BP.
XX
AC AAZ57637;
XX
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme, deltaRzPl.2 nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzPl.2; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT
FT stem_loop 7..19
FT /tag= b
FT /tag= c
FT misc_binding 20..25
FT /tag= c
FT /bound_moiety= "SPI.2 substrate bases (AAZ57634) 6-11"
FT
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-11"
FT
XX
XX W09955856-A2.
PN
XX
XX 04-NOV-1999.
PD
XX

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PF 29-APR-1999; 99WO-CA000391.
XX
PR 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
PS Example 1; Page; 52pp; English.
XX
CC This is the nucleotide sequence of ribozyme deltaRzPl.2. This ribozyme
CC cleaves substrate SPI.2 (see AAZ57634). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzPl.2) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'-GNHHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications. Note: This
CC sequence is not shown in the specification, but has been derived from the
CC deltaRzPl.1 sequence (AAZ57636) shown in figure 1
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match 95.7%; Score 35.4; DB 3; Length 57;
Best Local Similarity 73.0%; Pred. No. 0.42;
Matches 27; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCUCCGCGGUNNNNNNGGCAUGCBSY 37
Db 1 GGGUCCACCUCUCCGCGGCGGCCGACCGUCCGCAUGCCGC 37

RESULT 5
ADR47040
ID ADR47040 standard; DNA; 48 BP.
XX
XX ADR47040;
AC
XX
DT 18-NOV-2004 (first entry)
XX
DE Dengue virus vaccine oligonucleotide #15.
XX
XX ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
KW prem protein; C protein; NS1 protein signal; vaccine; cervical cancer;
KW viral disease; antigen; dendritic cell; immune response;
KW human papillomavirus.
XX
XX Unidentified.
OS
XX
XX WO2004072274-A1.
PN
XX
XX 26-AUG-2004.
PD
XX
XX 30-JAN-2004; 2004WO-CN000088.
PF
XX
XX 30-JAN-2003; 2003CN-00115272.
PR
XX
XX 30-JAN-2003; 2003CN-00115273.
PR
XX
XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA
XX
XX (TENG-) TENGGEN BIOMEDICAL CO.
PA
XX
XX (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX
XX Pang X;
PI

```

XX WPI; 2004-625870/60.
 XX Virus-like particle vaccines containing dengue virus recombinant replicon
 PT as core for carrier, applicable in preventives or/and remedies for tumors
 PT like cervical cancer and viral diseases.
 XX Example 4; SEQ ID NO 37; 38pp; Chinese.
 XX A dengue virus recombinant replicon has a deletion of the complete coding
 CC sequence for preM protein of dengue virus and also includes elements of
 CC e.g. the non-coding region in the whole of the 5'-end, the coding region
 CC of the front 20 amino acids in the C protein, and the coding region of
 CC NS1 protein signal; coding regions of all non-structural proteins. The
 CC obtained vaccines are useful in producing preventives or/and remedies for
 CC cancer like cervical cancer and viral diseases. Such vaccines can
 CC efficiently express antigen in infected cells, which is because dengue
 CC virus can infect dendritic cells, and can effectively present antigen to
 CC provide immunity effect. Different types of dengue virus can be used to
 CC repeatedly produce efficient immune response thereby strengthening the
 CC body's immune system against the pathogen that contains such antigen.
 CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
 CC expressing system using of the full-length dengue virus cDNA clone
 CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
 CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
 CC lines. This sequence corresponds to an oligonucleotide used in the
 CC recombinant replicon of the invention.
 XX Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
 SQ Query Match 81.1%; Score 30; DB 13; Length 48;
 Best Local Similarity 56.2%; Pred. No. 32;
 Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGUNNNNNNGGCGAUGCS 35
 Db :||||:||||:||||:||||:||||:|:
 17 TCCACCTCTCGCGTCCGACCTGGGCATCCG 48
 RESULT 6
 ADT48965
 ID ADT48965 standard; DNA; 48 BP.
 AC ADT48965;
 XX ADT48965;
 XX 16-DEC-2004 (first entry)
 DT PCR primer 5' HDVr, seq id 29.
 DE Virucide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;
 KW PCR; primer; ss.
 XX Viruses.
 OS WO2004082712-A1.
 PN 30-SEP-2004.
 PD 19-MAR-2004; 2004WO-CN000232.
 PF 20-MAR-2003; 2003CN-00115912.
 PR (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
 PA (TENG-) TENGGEN BIOMEDICAL CO.
 PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
 XX Pang X;
 XX WPI; 2004-699719/68.
 DR Bivalent vaccines for preventing and treating Japanese (B) encephalitis
 PT and hepatitis B produced by recombinant technique using encephalitis B
 PT virus as vector to express antigen gene of hepatitis B.

XX Example 8; SEQ ID NO 29; 33pp; Chinese.
 PS The invention relates to a recombinant Japanese encephalitis B virus
 CC constructed from encephalitis B virus and a recombinant genome, where the
 CC genome is inserted with an exogenous nucleotide sequence for
 CC recombination and capable of retaining its self-replication function. The
 CC virus is useful in producing the bivalent vaccines for preventing and
 CC treating Japanese (B) encephalitis and hepatitis B. Such vaccines are
 CC producible at low cost and have high immunoefficiency, in which the
 CC recombinant virus can efficiently express the antigen of hepatitis B
 CC virus with the safety and immunogenicity of attenuated encephalitis B
 CC virus vaccines. The current sequence represents a PCR primer used in an
 CC example from the invention.
 XX Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
 SQ Query Match 81.1%; Score 30; DB 13; Length 48;
 Best Local Similarity 56.2%; Pred. No. 32;
 Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGUNNNNNNGGCGAUGCS 35
 Db :||||:||||:||||:||||:||||:|:
 17 TCCACCTCTCGCGTCCGACCTGGGCATCCG 48
 RESULT 7
 AAQ86173
 ID AAQ86173 standard; DNA; 51 BP.
 XX AAQ86173;
 AC AAQ86173;
 XX 25-MAR-2003 (revised)
 DT 21-NOV-1995 (first entry)
 DE Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.
 XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX Synthetic.
 OS WO9507994-A2.
 PN 23-MAR-1995.
 PD 15-SEP-1994; 94WO-US010469.
 PF 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 XX (VIAG-) VIAGENE INC.
 XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
 PI WPI; 1995-131362/17.
 DR New alpha virus vectors for gene therapy - of viral infection, cancer,
 PT auto-immune disease, etc., and as vaccines.
 XX Example 2; Page 68; 260pp; English.
 PS The sequences given in AAQ86167-81 are primers which were used in the
 CC generation of plasmid DNA which initiates Sindbis infection. The
 CC amplified DNA sequences were used in the construction of a eukaryotic
 CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
 CC comprise a 5' sequence capable of initiating transcription of an
 CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
 CC proteins, a viral junction region which has been inactivated such that
 CC viral transcription of the subgenomic fragment is prevented, and an
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the viral

DT 12-SEP-1996 (first entry)
 XX HDV ribozyme primer HDV17-68.
 DE
 XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;
 KW polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;
 KW hepatitis delta virus; ss.
 XX Synthetic.
 XX
 PN WO9617072-A2.
 XX
 XX 06-JUN-1996.
 PD
 XX 30-NOV-1995; 95WO-US015490.
 PF
 XX 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00405827.
 XX
 PA (CHIR) CHIRON VIAGENE INC.
 XX Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;
 PI Belli BA;
 PI WPI; 1996-277785/28.
 DR
 XX New recombinant alpha-virus vectors - used to develop prods and methods
 PT for use in gene therapy and in the prodn. of vaccines.
 PT
 XX Example 3; Page 85; 256pp; English.
 PS
 CC Primer SHDV1F (AAT30816) contains a buffer sequence allowing enzyme
 CC digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme
 CC sequence. It was used with nested primer HDV17-68 (AAT30817) and reverse
 CC primer SHDV84R (AAT30818) to generate an HDV ribozyme. This antigenomic
 CC ribozyme can be placed between the polyA tract at the 3' end of a Sindbis
 CC virus-based eukaryotic layered vector initiation system, ELVIS, and the
 CC transcription terminal signals to produce alphavirus expression vectors
 CC useful in methods of gene therapy and for vaccine prodn
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 81.1%; Score 30; DB 2; Length 52;
 Best Local Similarity 56.2%; Pred. No. 33;
 Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 4 UCCACCUCUCGCGGUNNNNNNGGCGAUGCS 35
 :||||:||||:||||:||||:||||:||||:|
 Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
 RESULT 11
 AAV42394
 ID AAV42394 standard; DNA; 52 BP.
 XX
 AC AAV42394;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Forward PCR primer HDV17-68.
 XX
 KW DNA alphavirus; structural protein expression; inhibit; pathogen;
 KW immune response; stimulate; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX US5789245-A.
 PN
 PD 04-AUG-1998.
 XX
 DT 02-OCT-1998 (first entry)
 XX
 XX Nested PCR primer HDV17-68 of the invention.
 DE
 XX DNA alphavirus; structural protein expression; inhibit; pathogen;
 KW immune response; stimulate; PCR primer; ss.
 KW
 XX Synthetic.
 XX
 XX US5789245-A.
 PN
 XX 04-AUG-1998.
 PD
 XX 30-OCT-1996; 96US-00741881.
 PF
 XX

PR 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 30-NOV-1994; 94US-00348472.
 PR 20-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 PA (CHIR) CHIRON CORP.
 XX Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
 XX WPI; 1998-446089/38.
 DR
 XX DNA alpha:virus structural protein expression cassettes - for producing
 PT recombinant alpha:virus particles.
 PT
 XX Example 3; Col 69; 140pp; English.
 PS
 XX PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and an
 CC alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the cell,
 CC the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 81.1%; Score 30; DB 2; Length 52;
 Best Local Similarity 56.2%; Pred. No. 33;
 Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 4 UCCACCUCUCGCGGUNNNNNNGGCGAUGCS 35
 :||||:||||:||||:||||:||||:||||:|
 Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
 RESULT 12
 AAV42426
 ID AAV42426 standard; DNA; 52 BP.
 XX
 AC AAV42426;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Forward PCR primer HDV17-68.
 XX
 KW DNA alphavirus; structural protein expression; inhibit; pathogen;
 KW immune response; stimulate; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX US5789245-A.
 PN
 PD 04-AUG-1998.
 XX
 DT 02-OCT-1996; 96US-00741881.
 PF
 XX 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 30-NOV-1994; 94US-00348472.
 PR 20-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 PA (CHIR) CHIRON CORP.
 XX Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
 XX WPI; 1998-446089/38.
 DR
 XX DNA alpha:virus structural protein expression cassettes - for producing
 PT

PT recombinant alpha.virus particles.
 XX Example 7; Col 103; 140pp; English.
 XX
 CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and an
 CC alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the cell,
 CC the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 81.1%; Score 30; DB 2; Length 52;
 Best Local Similarity 56.2%; Pred. No. 33;
 Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUGCGGUNNNNNNGGCAUGCS 35
 :||||:||||:||||:||||:||||:|
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
 RESULT 13
 AAV60154
 ID AAV60154 standard; DNA; 52 BP.
 XX
 AC AAV60154;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 DE Nested PCR primer HDV17-68.
 XX
 XX Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis D virus.
 XX
 XX US5814482-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 30-OCT-1996; 96US-00739158.
 PF
 XX 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 XX (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 PI WPI; 1998-541753/46.
 XX
 XX Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 XX Example 3; Col 71-72; 144pp; English.
 PS
 XX PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
 CC ribozyme sequence. The product is used in the course of the invention.

CC The specification describes an eukaryotic layered vector initiation
 CC system, based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
 CC The RNA comprises a vector construct which autonomously amplifies in the
 CC cell and expresses a heterologous nucleic acid sequence which encodes an
 CC antigen or modified form that stimulates an immune response within an
 CC animal. The system is useful for stimulating an immune response to an
 CC antigen by introducing the vector into target cells, preferably by
 CC infection in vivo, especially where the immune response is a cell
 CC mediated, HLA class I-restricted or an HLA class II-restricted immune
 CC response. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 81.1%; Score 30; DB 2; Length 52;
 Best Local Similarity 56.2%; Pred. No. 33;
 Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUGCGGUNNNNNNGGCAUGCS 35
 :||||:||||:||||:||||:||||:|
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
 RESULT 14
 AAV60185
 ID AAV60185 standard; DNA; 52 BP.
 XX
 AC AAV60185;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 DE Reverse PCR primer HDV17-68.
 XX
 XX Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX US5814482-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 30-OCT-1996; 96US-00739158.
 PF
 XX 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 XX (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 PI WPI; 1998-541753/46.
 XX
 XX Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 XX Example 5; Col 108; 144pp; English.
 PS
 XX PCR primers AAV60184-85 are used in the course of the invention. The
 CC specification describes an eukaryotic layered vector initiation system,
 CC based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.

CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNNNGGCGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 15

AAV70746
ID AAV70746 standard; DNA; 52 BP.

XX
AC AAV70746;

XX
DT 20-MAR-2003 (revised)

DT 02-FEB-1999 (first entry)

XX Reverse PCR primer HDV17-68 used to amplify Hepatitis delta virus.

XX Alphavirus vector construct; gene therapy; PCR primer; ss.

XX Synthetic.

OS Hepatitis D virus.

XX US5843723-A.

XX 01-DEC-1998.

XX 30-OCT-1996; 96US-00739167.

XX 15-SEP-1993; 93US-00122791.

PR 18-FEB-1994; 94US-00198450.

PR 30-NOV-1994; 94US-00348472.

PR 20-JAN-1995; 95US-00376184.

PR 15-MAR-1995; 95US-00404796.

XX (CHIR) CHIRON CORP.

XX Chang SMW, Jolly DJ, Dubensky TW, Belli BA, Ibanez CE, Driver DA;

PI Polo JM;

XX WPI; 1999-044581/04.

XX Alphavirus vectors constructs containing a 5' promoter of viral cDNA by

PT in vitro transcription - used in gene therapy.

XX Example 7; Col 103; 140pp; English.

CC PCR primers AAV70745-46 are used to amplify part of the hepatitis delta
CC virus (HDV) genome. The amplified product is used in the production of
CC the alphavirus vector constructs of the invention. These constructs
CC comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA
CC from the viral cDNA by in vitro transcription, followed by a 5' sequence
CC which initiates transcription of alphavirus RNA, followed by a nucleotide
CC sequence encoding alphavirus nonstructural proteins, a viral junction
CC region which has been inactivated such that viral transcription of a
CC subgenomic fragment is prevented, an internal ribosome entry site or a
CC sequence which promotes ribosome read through between adjacent reading
CC frames, and an alphavirus RNA polymerase recognition sequence. The
CC recombinant alphavirus vectors can be used for gene therapy. (Updated on
CC 20-MAR-2003 to correct PR field.)

XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCCGCGGUNNNNNNGGCGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

Search completed: March 15, 2005, 16:13:06
Job time : 206.285 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:26:58 ; Search time 61.5044 Seconds
(without alignments)
984.356 Million cell updates/sec

Title: US-09-699-667E-65

Perfect score: 37

Sequence: 1 ggguccaccuccggunnnnnnnngggcaugcby 37

Scoring table: IDENTITY NUCDX

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/prodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCUS COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	81.1	52	1	US-08-741-881-40
2	30	81.1	52	1	US-08-741-881-80
3	30	81.1	52	1	US-08-739-158-40
4	30	81.1	52	1	US-08-739-158-80
5	30	81.1	52	2	US-08-739-167-40
6	30	81.1	52	2	US-08-739-167-80
7	30	81.1	52	3	US-08-404-796-40
8	30	81.1	52	3	US-08-404-796-80
9	30	81.1	52	3	US-08-931-869-40
10	30	81.1	52	3	US-08-931-869-80
11	30	81.1	52	3	US-09-350-399-40
12	30	81.1	52	3	US-09-350-399-80
13	30	81.1	52	3	US-09-236-140A-40
14	30	81.1	52	3	US-09-236-140A-80
15	29	78.4	56	3	US-09-415-784-39
16	29	78.4	56	3	US-09-415-785A-39
17	29	78.4	56	3	US-08-944-465-39
18	29	78.4	56	3	US-09-415-868-39
19	29	78.4	56	3	US-09-415-900-39
20	29	78.4	56	4	US-09-507-362-39
21	27	73.0	45	2	US-08-632-882-5
22	27	73.0	45	4	US-09-419-125-5
23	27	73.0	49	1	US-08-758-306-6
24	27	73.0	49	3	US-08-985-162-1875
25	27	73.0	49	3	US-08-998-099-373
26	27	73.0	49	3	US-09-112-086B-7
27	27	73.0	49	3	US-08-975-238-5

28	27	73.0	49	3	US-09-094-381C-18	Sequence 18, Appl
29	27	73.0	49	3	US-08-679-645-1234	Sequence 1234, Ap
30	27	73.0	49	3	US-09-676-807-9	Sequence 9, Appli
31	27	73.0	49	4	US-09-216-584-38	Sequence 38, Appl
32	27	73.0	49	4	US-09-812-186-5	Sequence 5, Appli
33	27	73.0	49	4	US-09-401-063-1875	Sequence 1875, Ap
34	24	64.9	52	1	US-08-238-963A-19	Sequence 19, Appl
C 35	23	62.2	58	3	US-08-646-695-40	Sequence 40, Appl
C 36	23	62.2	58	5	PCT-US96-06053-40	Sequence 10, Appl
C 37	22.6	61.1	35	3	US-08-894-727-10	Sequence 10, Appl
38	22.6	61.1	40	3	US-09-329-920-9	Sequence 9, Appli
39	22.4	60.5	39	3	US-08-485-355B-7	Sequence 7, Appli
40	22	59.5	33	2	US-08-888-366-32	Sequence 32, Appl
41	22	59.5	40	1	US-08-399-696-51	Sequence 51, Appl
C 42	22	59.5	47	1	US-08-244-626-18	Sequence 18, Appl
43	21.6	58.4	29	3	US-09-510-925A-8	Sequence 8, Appli
44	21.6	58.4	29	4	US-09-848-464-8	Sequence 8, Appli
45	21.4	57.8	39	3	US-08-978-806-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

Query Match 81.1%; Score 30; DB 1; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCGCGGNNNNNNNGGCGAUGCS 35

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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
      :|||||:|||||:|||||:|||||:|||||:|:
US-08-741-881-80
; Sequence 80, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-80
Query Match 81.1%; Score 30; DB 1; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCGAUGCS 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 3
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; Sequence 40, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-40
Query Match 81.1%; Score 30; DB 1; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCGAUGCS 35
      :|||||:|||||:|||||:|||||:|||||:|:
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 4
US-08-739-158-80
; Sequence 80, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80
Query Match 81.1%; Score 30; DB 1; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80

Query Match 81.1%; Score 30; DB 1; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 5

US-08-739-167-40
; Sequence 40, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-80

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 6

US-08-739-167-80
; Sequence 80, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-80

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 7

US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
US-08-739-167-80

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-80

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 7

US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-80

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 7

US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
US-08-739-167-80

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 7

US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
US-08-739-167-80

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 7

US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
US-08-739-167-80

/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/404,796
/ FILING DATE: 15-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-404-796-40

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
DB 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 8
US-08-404-796-80
/ Sequence 80, Application US/08404796
/ Patent No. 6015686
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/404,796
/ FILING DATE: 15-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear

US-08-404-796-80
Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
DB 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 9
US-08-931-869-40
/ Sequence 40, Application US/08931869
/ Patent No. 6015694
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/931,869
/ FILING DATE: 16-SEP-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/404,796
/ FILING DATE: 15-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-931-869-40

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCAUGCS 35
:||||:||||:||||:||||:||||:|
DB 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 10
US-08-931-869-80
/ Sequence 80, Application US/08931869
/ Patent No. 6015694
/ GENERAL INFORMATION:

APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Dubensky Jr, Thomas W
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-80

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCGCGGCGGNNNNNGGCGAUGCS 35
:|||||:|||||:|||||:|||||:|
Db 1 TCCACCTCTCGGCTCCGACCTGGCGCATCCG 32

RESULT 11
US-09-350-399-40
Sequence 40, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Dubensky Jr, Thomas W
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-350-399-80

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Dubensky Jr, Thomas W
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-350-399-40

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCGCGGCGGNNNNNGGCGAUGCS 35
:|||||:|||||:|||||:|||||:|
Db 1 TCCACCTCTCGGCTCCGACCTGGCGCATCCG 32

RESULT 12
US-09-350-399-80
Sequence 80, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Dubensky Jr, Thomas W
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-350-399-80

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCGCAUGCS 35
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DB 1 TCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 13

US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-236-140A-40

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCGCAUGCS 35
:||||:||||:||||:||||:||||:|
DB 1 TCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 14

US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.

Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:

US-09-236-140A-80

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCGCAUGCS 35
:||||:||||:||||:||||:||||:|
DB 1 TCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 15

US-09-415-784-39
; Sequence 39, Application US/09415784
; Patent No. 6391632
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolow, Ilya

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-415-784-39

Query Match 78.4%; Score 29; DB 3; Length 56;
Best Local Similarity 58.6%; Pred. No. 19;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
Qy 4 UCCACCUCCUCGCGGNNNNNNNGGCAU 32
Db 27 TCCACCTCTCGGGGTCCGACCTGGGCAT 55

Search completed: March 15, 2005, 20:44:24
Job time : 61.5044 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:26:58 ; Search time 61.5044 Seconds
(without alignments)
984.356 Million cell updates/sec

Title: US-09-699-667E-63
Perfect score: 37
Sequence: 1 ggguccaccuccgcggunnnmnnuggcgcc 37

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30.4	82.2	52	1	US-08-741-881-80
3	30.4	82.2	52	1	US-08-739-158-40
4	30.4	82.2	52	1	US-08-739-158-80
5	30.4	82.2	52	2	US-08-739-167-40
6	30.4	82.2	52	2	US-08-739-167-80
7	30.4	82.2	52	3	US-08-404-796-40
8	30.4	82.2	52	3	US-08-404-796-80
9	30.4	82.2	52	3	US-08-931-869-40
10	30.4	82.2	52	3	US-08-931-869-80
11	30.4	82.2	52	3	US-09-350-399-40
12	30.4	82.2	52	3	US-09-350-399-80
13	30.4	82.2	52	3	US-09-326-140A-40
14	30.4	82.2	52	3	US-09-326-140A-80
15	29	78.4	56	3	US-09-415-784-39
16	29	78.4	56	3	US-09-415-785A-39
17	29	78.4	56	3	US-08-944-465-39
18	29	78.4	56	3	US-09-415-868-39
19	29	78.4	56	3	US-09-415-900-39
20	29	78.4	56	4	US-09-507-362-39
21	24	64.9	52	1	US-08-238-963A-19
22	23	62.2	58	3	US-08-646-695-40
23	23	62.2	58	5	PCT-US96-06053-40
24	22.4	60.5	39	3	US-08-485-3558-7
25	22	59.5	45	2	US-08-632-882-5
26	22	59.5	45	4	US-09-419-125-5
27	22	59.5	49	1	US-08-758-306-6

28	22	59.5	49	3	US-08-985-162-1875	Sequence 1875, Ap
29	22	59.5	49	3	US-08-998-099-373	Sequence 373, Appl
30	22	59.5	49	3	US-09-112-086B-7	Sequence 7, Appli
31	22	59.5	49	3	US-08-975-238-5	Sequence 5, Appli
32	22	59.5	49	3	US-09-094-381C-18	Sequence 18, Appl
33	22	59.5	49	3	US-08-679-645-1234	Sequence 1234, Ap
34	22	59.5	49	3	US-09-676-807-9	Sequence 9, Appli
35	22	59.5	49	4	US-09-216-584-38	Sequence 38, Appl
36	22	59.5	49	4	US-09-812-186-5	Sequence 5, Appli
37	22	59.5	49	4	US-09-401-063-1875	Sequence 1875, Ap
C 38	21	56.8	21	6	5225337-3	Patent No. 5225337
C 39	21	56.8	21	6	5225337-3	Patent No. 5225337
C 40	21	56.8	35	3	US-08-894-727-10	Sequence 10, Appl
41	21	56.8	40	3	US-09-329-920-9	Sequence 9, Appli
42	20.8	56.2	44	4	US-08-150-204E-44	Sequence 44, Appl
43	20.4	55.1	33	2	US-08-888-366-32	Sequence 32, Appl
44	20.4	55.1	37	4	US-09-649-747A-59	Sequence 59, Appl
C 45	20.4	55.1	47	1	US-08-244-626-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr. Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

Query Match 82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCGCGGGUNNNNNUGGCGAUGCG 35

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Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
      :|||||:|||||:|||||:|||||:|||||:
RESULT 2
US-08-741-881-80
; Sequence 80, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-80
Query Match 82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
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RESULT 3
US-08-739-158-40
; Sequence 40, Application US/08739158
; Patent No. 581482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-40
Query Match 82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNUGGCGAUGC 35
      :|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
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STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,158
FILING DATE: 30-OCT-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-158-40
Query Match 82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
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RESULT 4
US-08-739-158-80
; Sequence 80, Application US/08739158
; Patent No. 581482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80
Query Match 82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNUGGCGAUGC 35
      :|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80

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Query Match 82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy	4 UCCACCUCCUCGCGUNNNNNUGGCAUGC G 35 : : : : :
Db	1 TCCACCTCCTCGCGGTCCGACCCTGGGCATCCG 32 : : : : :

RESULT 5
 US-08-739-167-40
 ; Sequence 40, Application US/08739167
 ; Patent No. 5843723
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubensky Jr, Thomas W
 ; APPLICANT: Polo, John M.
 ; APPLICANT: Ibanez, Carlos E.
 ; APPLICANT: Chang, Stephen M.W.
 ; APPLICANT: Jolly, Douglas J.
 ; APPLICANT: Driver, David A.
 ; APPLICANT: Belli, Barbara A.
 ; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
 ; NUMBER OF SEQUENCES: 128
 ; CORRESPONDENCE ADDRESS:

ADDRESS: 6300 and DEAR LUF
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington

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; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/739,167
/ FILING DATE: 30-OCT-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:

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/ ..... case pair
/
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/

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Query Match	82.2%;	Score 30.4; DB
Best Local Similarity	59.4%;	Pred. No. 4.2;

Qy 4 UCCACCUCCGCGGUNNNNNUGGCGAUGCG 35
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db 1 TCCACCTCCTCGCGTCCGACCTGGGCATCG 32

RESULT 6
US-08-739-167-80
; Sequence 80, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McWasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-404-796-40

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUCG 35
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 8
US-08-404-796-80
; Sequence 80, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McWasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-404-796-80
Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUCG 35
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 9
US-08-931-869-40
; Sequence 40, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McWasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-931-869-40

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUCG 35
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 10
US-08-931-869-80
; Sequence 80, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:

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; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-931-869-80

Query Match      82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy      4 UCCACUCCUCCGCGGNNNNNUGGCGAUCG 35
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Db      1 TCCACCTCTCGCGGTCGCGACCTGGGCATCCG 32

RESULT 11
US-09-350-399-40
; Sequence 40, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
;           Polo, John M.
;           Jolly, Douglas J.
;           Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-350-399-80
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-350-399-40

Query Match      82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy      4 UCCACUCCUCCGCGGNNNNNUGGCGAUCG 35
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Db      1 TCCACCTCTCGCGGTCGCGACCTGGGCATCCG 32

RESULT 12
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
;           Polo, John M.
;           Jolly, Douglas J.
;           Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-350-399-80
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Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 13

US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-236-140A-40
Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 14

US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.

Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100
INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80
Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15

US-09-415-784-39
; Sequence 39, Application US/09415784
; Patent No. 6391632
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-415-784-39

Query Match 78.4%; Score 29; DB 3; Length 56;
Best Local Similarity 58.6%; Pred. No. 13;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
QY 4 UCCACCUCCUCGCGGUNNNNNUGGCAU 32
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REFERENCE
AUTHORS
Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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LOCUS
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DEFINITION
Sequence 47 from Patent WO995856.
ACCESSION
AX012285
VERSION
AX012285.1 GI:9998346
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SOURCE
synthetic construct
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other sequences; artificial sequences.
REFERENCE
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AUTHORS
Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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DEFINITION
Sequence 48 from Patent WO995856.
ACCESSION
AX012286
VERSION
AX012286.1 GI:9998347
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
other sequences; artificial sequences.
1
REFERENCE
AUTHORS
Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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source
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/notes="synthetic nucleic acid"
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Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
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AX012287 57 bp RNA linear PAT 06-SEP-2000
DEFINITION
Sequence 49 from Patent WO995856.
ACCESSION
AX012287
VERSION
AX012287.1 GI:9998348
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 49 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Location/Qualifiers
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/organism="synthetic construct"
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/notes="synthetic nucleic acid"
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Query Match
Best Local Similarity 100.0%; Score 57; DB 6; Length 57;
Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCCGCGGNNNNNUGGCGAUGCGGCUUCGCAUGGCUAAGGACCC 57
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RESULT 6
AX012288
LOCUS
AX012288 57 bp RNA linear PAT 06-SEP-2000
DEFINITION
Sequence 50 from Patent WO995856.
ACCESSION
AX012288
VERSION
AX012288.1 GI:9998349
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 50 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="synthetic nucleic acid"
ORIGIN
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Query Match 100.0%; Score 57; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 2.3e-05;
Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
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RESULT 7
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LOCUS AX012289 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION AX012289
VERSION AX012289.1 GI:9998350
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Query Match 100.0%; Score 57; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 2.3e-05;
Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
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Db 1 GGGTCCACCTCTCGCGGTCCGAGCTGGCATCGGCTTCGCATGGCTAAGGACCC 57

RESULT 8
AX012290
LOCUS AX012290 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION AX012290
VERSION AX012290.1 GI:9998351
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 52 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 57; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 2.3e-05;
Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
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RESULT 9
AX012284
LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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/mol_type="unassigned RNA"
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/note="synthetic nucleic acid"

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LOCUS AX012291 37 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 53 from Patent WO9955856.
ACCESSION AX012291
VERSION AX012291.1 GI:9998352
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 53 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="synthetic nucleic acid"

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RESULT 11
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LOCUS AR021007 52 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 40 from patent US 5789245.

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ACCESSION AR021007
VERSION AR021007.1 GI:3975622
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 5789245-A 40 04-AUG-1998;
FEATURES
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        /mol_type="unassigned DNA"
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Best Local Similarity 59.4%; Pred. No. 3.1e+03;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUCG 35
Db 1 TCACCTCTCTCGCGTCCGACCTGGGCATCCG 32
RESULT 14
LOCUS AR043462
DEFINITION Sequence 80 from patent US 5814482.
ACCESSION AR043462
VERSION AR043462.1 GI:5964470
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 80 29-SEP-1998;
FEATURES
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Query Match 53.3%; Score 30.4; DB 6; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.1e+03;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUCG 35
Db 1 TCACCTCTCTCGCGTCCGACCTGGGCATCCG 32
RESULT 15
LOCUS AR062337
DEFINITION Sequence 40 from patent US 5843723.
ACCESSION AR062337
VERSION AR062337.1 GI:5990028
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W.,
TITLE Jolly,D.J., Driver,D.A. and Belli,B.A.
JOURNAL Alphavirus vector constructs
Patent: US 5843723-A 40 01-DEC-1998;
FEATURES
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        /mol_type="unassigned DNA"
ORIGIN
Query Match 53.3%; Score 30.4; DB 6; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.1e+03;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUCG 35
Db 1 TCACCTCTCTCGCGTCCGACCTGGGCATCCG 32
RESULT 13
LOCUS AR043422
DEFINITION Sequence 40 from patent US 5814482.
ACCESSION AR043422
VERSION AR043422.1 GI:5964430
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 40 29-SEP-1998;
FEATURES
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-699-667E-66

Perfect score: 20

Sequence: 1 bksgcauggcuaggagacc 20

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Searched: 1202784 seqs, 81813359 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.8	79.0	601	4	US-09-949-016-18503
C 2	15.8	79.0	601	4	US-09-949-016-176107
C 3	15.8	79.0	11725	2	US-08-756-506-1
C 4	15.8	79.0	11725	4	US-09-328-925-50
C 5	15.8	79.0	11725	4	US-09-054-272-31
C 6	15.8	79.0	14802	4	US-09-949-016-16753
C 7	15.4	77.0	3595	4	US-09-949-016-4833
C 8	15.4	77.0	25198	4	US-09-949-016-18575
C 9	15.4	77.0	818128	4	US-09-949-016-14546
C 10	15.4	77.0	818128	4	US-09-949-016-14547
C 11	15.4	77.0	818128	4	US-09-949-016-14548
C 12	15.4	77.0	818128	4	US-09-949-016-14549
C 13	15.4	77.0	818128	4	US-09-949-016-14550
C 14	15.4	77.0	818128	4	US-09-949-016-14551
C 15	15.4	77.0	818128	4	US-09-949-016-14552
C 16	15.4	77.0	818128	4	US-09-949-016-14553
C 17	15.4	77.0	818128	4	US-09-949-016-14554
C 18	15.4	77.0	818128	4	US-09-949-016-14555
C 19	15.4	77.0	818128	4	US-09-949-016-14556
C 20	15.4	77.0	818128	4	US-09-949-016-14557
C 21	15.4	77.0	818128	4	US-09-949-016-14558
C 22	15.4	77.0	818128	4	US-09-949-016-14559
C 23	15.4	77.0	818128	4	US-09-949-016-14560
C 24	15.4	77.0	818128	4	US-09-949-016-14561
C 25	15.4	77.0	818128	4	US-09-949-016-14562
C 26	15.4	77.0	818128	4	US-09-949-016-14564
C 27	15.4	77.0	818128	4	US-09-949-016-14565

C 28	15.4	77.0	818128	4	US-09-949-016-14566	Sequence 14566, A
C 29	15.4	77.0	818128	4	US-09-949-016-14567	Sequence 14567, A
C 30	15.2	76.0	215	4	US-09-513-999C-17447	Sequence 17447, A
C 31	15.2	76.0	3986	3	US-09-053-374A-3	Sequence 3, Appli
C 32	15.2	76.0	52789	4	US-09-949-016-12130	Sequence 12130, A
C 33	15.2	76.0	52790	4	US-09-949-016-16641	Sequence 16641, A
C 34	15.2	76.0	60304	4	US-09-949-016-11995	Sequence 11995, A
C 35	15.2	76.0	60304	4	US-09-949-016-17264	Sequence 17264, A
C 36	15.2	76.0	79578	4	US-09-949-016-16339	Sequence 16339, A
C 37	15.2	76.0	97221	4	US-09-949-016-12755	Sequence 12755, A
C 38	15.2	76.0	141248	4	US-09-949-016-12241	Sequence 12241, A
C 39	15.2	76.0	143248	4	US-09-949-016-16652	Sequence 16652, A
C 40	15	75.0	439	3	US-09-397-787-313	Sequence 313, App
C 41	15	75.0	573	3	US-08-936-165A-48	Sequence 48, Appl
C 42	15	75.0	14871	4	US-09-949-016-13013	Sequence 13013, A
C 43	14.4	72.0	39	1	US-08-096-027-4	Sequence 4, Appli
C 44	14.4	72.0	39	1	US-08-461-725-4	Sequence 4, Appli
C 45	14.4	72.0	39	2	US-08-460-981-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-18503/c
; Sequence 18503, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18503
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-18503

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 1.1e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAGGACC 19
DB 523 GCGCATGCGCAAGGACC 505

RESULT 2

US-09-949-016-176107/c
; Sequence 176107, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176107
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-176107

Query Match          79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 1.1e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1  BKSGCAUGGCUAAGGACC 19
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Db      523  GCGCATGGCAAAGGACC 505
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RESULT 3
US-08-756-506-1/c
; Sequence 1, Application US/08/756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Cottingham, Ian R.
; APPLICANT: Temperley, Simon M.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prunkard, Donna E.
; TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
; TITLE OF INVENTION: ANIMALS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,506
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 95-28
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(3520..3630, 5093..5117, 5210..5347, 5450
; LOCATION: ..5584, 8253..8395, 9269..9386, 10516..11102)
; US-08-756-506-1

Query Match          79.0%; Score 15.8; DB 2; Length 11725;
Best Local Similarity 73.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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; INFORMATION FOR SEQ ID NO: 31:
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; LENGTH: 11725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-054-272-31

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Best Local Similarity 73.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19
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RESULT 6

US-09-949-016-16753/c
; Sequence 16753, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16753
; LENGTH: 14802
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(14802)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16753

Query Match 79.0%; Score 15.8; DB 4; Length 14802;
Best Local Similarity 73.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19
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Db 2247 GCGCATGGCAAAAGGACC 2229

RESULT 7

US-09-949-016-4833
; Sequence 4833, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4833
; LENGTH: 3595
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4833

Query Match 77.0%; Score 15.4; DB 4; Length 3595;
Best Local Similarity 82.4%; Pred. No. 2.1e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 20
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Db 2520 GCATGGCTGAGGACC 2536

RESULT 8

US-09-949-016-16575
; Sequence 16575, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16575
; LENGTH: 25198
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(25198)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16575

Query Match 77.0%; Score 15.4; DB 4; Length 25198;
Best Local Similarity 82.4%; Pred. No. 2.5e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 20
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Db 22122 GCATGGCTGAGGACC 22138

RESULT 9

US-09-949-016-14546/c
; Sequence 14546, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14546
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14546

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Query Match	77.0%	Score 15.4;	DB 4;	Length 818128;
Best Local Similarity	70.6%	Pred. No. 3.2e+02;		
Matches 12;	Conservative	5;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 1 B K S G C A U G G C U A A G G G A 17
:::|:::|:::|:::|:::|:::|
Db 248008 C T G G C A T G G C T A A G G G A 247992

```

RESULT 10
US-09-949-016-14547/c
; Sequence 14547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14547
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14547

```

Query Match	77.0%	Score 15.4;	DB 4;	Length 818128;
Best Local Similarity	70.6%	Pred. No. 3.2e+02;		
Matches 12;	Conservative	5;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 1 BKSGCAUGGCUAAGGGA 17
:::|::|::|::|::|
Db 248008 CTGGCATGGCTAAGGGA 247992

RESULT 11
 US-09-949-016-14548/c
 ; Sequence 14548, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03

```

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14548
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14548

```

Query Match	77.0%	Score 15.4	DB 4	Length 818128
Best Local Similarity	70.8%	Pred. No. 3.2e+02		
Matches 12	Conservative 5	Mismatches 0	Indels 0	Gaps 0

QY 1 EKSGCAUGGCUAAGGGA 17
:::|::|::|::|::|::|
Db 248008 CTGGCATGGCTAAGGGA 247992

RESULT 12
US-09-949-016-14549/c
; Sequence 14549, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14549
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14549

Query Match	77.0%	Score 15.4	DB 4	Length 818128
Best Local Similarity	70.6%	Pred. No. 3.2e+02		
Matches 12	Conservative	5	Mismatches 0	Indels 0
				Gaps 0

Qy 1 BKSGCAUGGCUAAGGA 17
:::|::|::|::|::|
Db 248008 CTGGCATGGCTAAGGA 247992

RESULT 13
 US-09-949-016-14550/c
 ; Sequence 14550, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14550
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14550

Query Match 77.0%; Score 15.4; DB 4; Length 818128;
Best Local Similarity 70.6%; Pred. No. 3.2e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGGA 17
Db 248008 CTGGCATGCGTAAGGGA 247992

RESULT 14
US-09-949-016-14551/c
; Sequence 14551, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14551
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14551

Query Match 77.0%; Score 15.4; DB 4; Length 818128;
Best Local Similarity 70.6%; Pred. No. 3.2e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGGA 17
Db 248008 CTGGCATGCGTAAGGGA 247992

RESULT 15
US-09-949-016-14552/c
; Sequence 14552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14552
; LENGTH: 818128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14552

Query Match 77.0%; Score 15.4; DB 4; Length 818128;
Best Local Similarity 70.6%; Pred. No. 3.2e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGGA 17
Db 248008 CTGGCATGCGTAAGGGA 247992

Search completed: March 15, 2005, 15:26:52
Job time : 45.1579 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:20:59 ; Search time 804.561 Seconds
(without alignments)
946.212 Million cell updates/sec

Title: US-09-699-667E-66

Perfect score: 20

Sequence: 1 bksgaugcuaaggagacc 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gse1: *
9: gb_gse2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12.8	64.0	40	9	AL763075	AL763075 Arabidops
2	12.8	64.0	58	9	CR183540	CR183540 Forward s
3	12.6	63.0	40	1	AI316323	AI316323 u199b12.y
4	12.6	63.0	56	9	CG715094	CG715094 l119039H0
5	12.4	62.0	34	8	AZ876899	AZ876899 2M0192C06
6	12.4	62.0	46	1	AI937668	AI937668 wp82b01.x
7	12.4	62.0	51	9	CL256773	CL256773 X50948 Sa
8	12.2	61.0	26	8	AZ804424	AZ804424 2M0065C11
9	12.2	61.0	54	9	AL940566	AL940566 Arabidops
10	12.0	60.0	23	4	BM394673	BM394673 50072-2.5
11	12.0	60.0	23	8	AZ658079	AZ658079 IM0534H11
12	12.0	60.0	27	4	BM395243	BM395243 50072-2.8
13	12.0	60.0	29	8	AZ820217	AZ820217 2M0092I13
14	12.0	60.0	34	8	BH789679	BH789679 SALK_0444
15	12.0	60.0	36	9	AL771940	AL771940 Arabidops
16	12.0	60.0	38	9	AL771951	AL771951 Arabidops
17	12.0	60.0	42	9	EX997261	EX997261 Arabidops
18	12.0	60.0	50	8	BH811451	BH811451 SALK_0586
19	12.0	60.0	51	9	EX291747	EX291747 Arabidops
20	12.0	60.0	52	4	BM393985	BM393985 50072-2.1
21	12.0	60.0	52	9	EX990873	EX990873 Arabidops
22	12.0	60.0	56	6	CB274124	CB274124 mai89all.
23	12.0	60.0	59	1	AI633365	AI633365 t896c12.x
24	12.0	60.0	59	9	AL944166	AL944166 Arabidops

C	25	12	60.0	60	9	CL211870	CL211870 W084D04 G
	26	11.8	59.0	27	4	BM395141	BM395141 50072-2-7
	27	11.8	59.0	31	9	AL770473	AL770473 Arabidops
C	28	11.8	59.0	43	8	CC178564	CC178564 NPX457 Ba
	29	11.8	59.0	48	9	EX291304	EX291304 Arabidops
	30	11.8	59.0	48	9	TA254C04P	TA254C04P T. brucei
	31	11.8	59.0	50	1	AU105803	AU105803 AU105803
C	32	11.8	59.0	50	8	AZ452836	AZ452836 IM0252H23
	33	11.8	59.0	51	9	AL940176	AL940176 Arabidops
C	34	11.8	59.0	51	9	CR221046	CR221046 Forward s
	35	11.8	59.0	52	8	AZ628524	AZ628524 IM0480J11
	36	11.8	59.0	52	9	AL761298	AL761298 Arabidops
C	37	11.8	59.0	60	7	H52868	H52868 EST0022 Tes
	38	11.8	59.0	60	9	EX532971	EX532971 Arabidops
C	39	11.8	59.0	60	9	EX979387	EX979387 Reverse s
	40	11.6	58.0	51	9	EX533437	EX533437 Arabidops
	41	11.6	58.0	53	4	BJ059689	BJ059689 BJ059689
	42	11.6	58.0	55	8	CC049927	CC049927 O1S0518-0
C	43	11.6	58.0	56	9	CG705810	CG705810 O1S0588-1
	44	11.6	58.0	57	4	BM127716	BM127716 Ie98H06.Y
	45	11.6	58.0	59	8	AZ487775	AZ487775 IM0317I12

ALIGNMENTS

RESULT 1	AL763075	40 bp	DNA	linear	GSS 01-APR-2004
LOCUS	Arabidopsis thaliana T-DNA flanking sequence	Arabidopsis thaliana T-DNA flanking sequence	GK-032C06-014864,		
DEFINITION	genomic survey sequence.				
ACCESSION	AL763075				
VERSION	AL763075.1	GI:21511171			
KEYWORDS	GSS.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE 1	Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.				
AUTHORS	GABI-kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana				
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)				
MEDLINE	22755829				
PUBMED	12874060				
REFERENCE 2	Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.				
AUTHORS	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics				
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)				
MEDLINE	23117147				
PUBMED	14756321				
REFERENCE 3	Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.				
AUTHORS	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines				
JOURNAL	Biotechniques 35 (6), 1164-1168 (2003)				
MEDLINE	14682050				
PUBMED					
REFERENCE 4	(bases 1 to 40)				
AUTHORS	Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.				
JOURNAL	Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany				
MEDLINE	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g21630.				
PUBMED	Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.				
AUTHORS	GABI-Kat is part of the German Plant Genomics program designated				

'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source
Location/Qualifiers
1. .40
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="CK-032C06-014864"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/cotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 64.0%; Score 12.8; DB 9; Length 40;
Best Local Similarity 75.0%; Pred. No. 7.4e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAUGGCUAAGGGACCC 20
||:||||:||||||
Db 25 CATGGCTATGGGATCC 40

RESULT 2

CR183540/c
LOCUS
DEFINITION
Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN121h03, genomic survey sequence.
CR183540
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITILE
JOURNAL
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
1. .58
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN121h03"
/clone_lib="MHPN"

FEATURES

source
Query Match 64.0%; Score 12.8; DB 9; Length 58;
Best Local Similarity 77.8%; Pred. No. 7.8e+04;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SGCAUGGCUAAGGGACCC 20
:||||:|||||||
Db 42 GGCACGGAGAGGGACCC 25

ORIGIN

RESULT 3
AI1316323/c
LOCUS
DEFINITION
uJ99b12.y1 Schiller mouse MAC13 Mus musculus cDNA clone IMAGE:1958015 5' similar to TR:035934 035934 CLN3. ;, mRNA sequence.
AI1316323
ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

AI1316323.1 GI:4031590
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 40)
REFERENCE
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE JOURNAL COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:984355

FEATURES

source
1. .40
/organism="Mus musculus"
/mol_type="mrna"
/db_xref="taxon:10090"
/clone="IMAGE:1958015"
/tissue type="colon cancer"
/cell_lines="colon cancer cell line MAC13"
/lab host="SOLR"
/clone_lib="Schiller mouse MAC13"
/note="Vector: pBluescript SK- (Stratagene); Site 1: EcoRI; Site 2: XhoI; Double-stranded cDNA was prepared from cell line MAC13 using primer 5'-GAGAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATTCGACGACGAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."
Query Match 63.0%; Score 12.6; DB 1; Length 40;
Best Local Similarity 64.7%; Pred. No. 9.3e+04;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17
:::||||:||||
Db 27 TGAGCATGGCTAGGGA 11

ORIGIN

Query Match 63.0%; Score 12.6; DB 1; Length 40;
Best Local Similarity 64.7%; Pred. No. 9.3e+04;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17
:::||||:||||
Db 27 TGAGCATGGCTAGGGA 11

RESULT 4
CG715094
LOCUS
DEFINITION
1119039H08.xl 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
CG715094
VERSION
CG715094.1 GI:37742080
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 56)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
JOURNAL
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 119039 row: H column: 08
Class: transposon-tagged.
Location/Qualifiers
1. 56
/organism="Zea mays"
/mol_type="genomic DNA"
/culturvar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES
source

ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 56;
Best Local Similarity 73.3%; Pred. No. 9.8e+04;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGG 16
:::|||||
Db 8 TGGCATGCCCAAGG 22

RESULT 5
AZ876899
LOCUS
DEFINITION
2M0192C06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC2M0192C06 F, genomic survey sequence.
ACCESSION
VERSION
AZ876899
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weisse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 56)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
JOURNAL
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 119039 row: H column: 08
Class: transposon-tagged.
Location/Qualifiers
1. 56
/organism="Zea mays"
/mol_type="genomic DNA"
/culturvar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES
source

ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 56;
Best Local Similarity 73.3%; Pred. No. 9.8e+04;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGG 16
:::|||||
Db 8 TGGCATGCCCAAGG 22

RESULT 5
AZ876899
LOCUS
DEFINITION
2M0192C06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC2M0192C06 F, genomic survey sequence.
ACCESSION
VERSION
AZ876899
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weisse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 56)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
JOURNAL
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 119039 row: H column: 08
Class: transposon-tagged.
Location/Qualifiers
1. 56
/organism="Zea mays"
/mol_type="genomic DNA"
/culturvar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES
source

ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 56;
Best Local Similarity 73.3%; Pred. No. 9.8e+04;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGG 16
:::|||||
Db 8 TGGCATGCCCAAGG 22

RESULT 5
AZ876899
LOCUS
DEFINITION
2M0192C06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC2M0192C06 F, genomic survey sequence.
ACCESSION
VERSION
AZ876899
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weisse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 56)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
JOURNAL
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 119039 row: H column: 08
Class: transposon-tagged.
Location/Qualifiers
1. 56
/organism="Zea mays"
/mol_type="genomic DNA"
/culturvar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES
source

ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 56;
Best Local Similarity 73.3%; Pred. No. 9.8e+04;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGG 16
:::|||||
Db 8 TGGCATGCCCAAGG 22

RESULT 5
AZ876899
LOCUS
DEFINITION
2M0192C06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC2M0192C06 F, genomic survey sequence.
ACCESSION
VERSION
AZ876899
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weisse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio1.lni.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES

source
Location/Qualifiers

1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2468233"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCATCTGAAGTGGAGCGCGCATAGGTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 62.0%; Score 12.4; DB 1; Length 46;
Best Local Similarity 64.3%; Pred. No. 1.2e+05;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 BKSGCAUGGCUAAG 14
DB 28 TTGGCATGGCTAAG 15

RESULT 7

CL256773/c
LOCUS XS0948 Sanger Institute Gene Trap Library pGT01xf Mus musculus
DEFINITION 51 bp mRNA linear GSS 02-FEB-2004
CDNA, mRNA sequence.

CL256773

CL256773.1 GI:41620565

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 51)

Sanger Institute Gene Trap Resource - SIGTR.

<http://www.sanger.ac.uk/PostGenomics/genetrp/>

Unpublished (2003)

Contact: Sanger Institute Gene Trap Resource - SIGTR

Wellcome Trust Sanger Institute

Email: info.genetraps@sanger.ac.uk

Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
<http://www.sanger.ac.uk/PostGenomics/genetrp/>
Class: Gene Trap

FEATURES

source
Location/Qualifiers

1..51
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xf"
/note="Vector: pGT01xf"

ORIGIN

Query Match 62.0%; Score 12.4; DB 9; Length 51;
Best Local Similarity 72.2%; Pred. No. 1.2e+05;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 KSGCAUGGCUAAGGACC 19

DB 47 GGCCACGGCGAAGGACC 30

RESULT 8

AZ804424/c

LOCUS AZ804424

DEFINITION 2M0065C11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0065C11 F, genomic survey sequence.

ACCESSION AZ804424

VERSION AZ804424.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Isilam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0065 row: C column: 11

Seq primer: CTTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source
Location/Qualifiers

1..26
/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0065C11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: H column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0534H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 23;
Best Local Similarity 55.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGACCC 20
:::||||:|||||

DB 22 CTGGCATAGTCAGGACGC 3

RESULT 12 BM395243

LOCUS BM395243

DEFINITION 50072-2-8-B11.r.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395243

VERSION BM395243.1 GI:18195296

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 27)

REFERENCE

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES Location/Qualifiers
1..27
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 60.0%; Score 12; DB 4; Length 27;
Best Local Similarity 55.0%; Pred. No. 1.8e+05;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGACCC 20
:::||||:|||||

DB 5 GCGCAATGGGTACGGGCCCC 24

RESULT 13 AZ820217

LOCUS AZ820217

DEFINITION 2M0092113F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0092113 F, genomic survey sequence.

ACCESSION AZ820217

VERSION AZ820217.1 GI:12990125

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss

COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: I column: 13
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.

FEATURES Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0092113"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 29;
 Best Local Similarity 60.0%; Pred. NO. 1.8e+05;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20
 ::::|||||
 Db 21 TTCGCATAGGAGGGACCC 2

RESULT 14

BH789679

LOCUS 34 bp DNA linear GSS 02-APR-2002
 DEFINITION Arabidopsis thaliana T-DNA insertion lines
 Arabidopsis thaliana genomic clone SALK_044456.15.50.n, genomic survey sequence.

ACCESSION BH789679

VERSION 1 GI:19882777

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 34)

AUTHORS

Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Arabidopsis Genome

COMMENT Unpublished (2001)

Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
 Fax: 858 538 6379

Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of

TDNA.
 Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..34

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_044456.15.50.n"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 34;
 Best Local Similarity 71.4%; Pred. NO. 1.8e+05;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGCAUGGCUAAGG 16
 :|||:|||||
 Db 10 GGATGCGTAACGG 23

RESULT 15

AL771940

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-184G03-013649,
 genomic survey sequence.

ACCESSION AL771940

VERSION AL771940.1 GI:21534142

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

TITLE

Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 Weissshaar,B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Li,Y., Rosso,M.G., Strizhov,N. and Weissshaar,B.
 Direct Submission
 Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion close to or within gene At5g24260.
 Details on the protocols used for generation of the sequence are
 described in References 1-3. The sequences are generated at the MPI
 for Plant Breeding Research in the context of the GABI-Kat project.
 GABI-Kat is part of the German Plant Genomics program designated
 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

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Location/Qualifiers

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/db_xref="taxon:3702"

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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"
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 vector PAC161 (Genbank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

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 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20
 DB 17 TTGGCACCGCTATGGATCC 36

Search completed: March 15, 2005, 20:38:26
 Job time : 813.561 secs

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4	47.4	83.2	57	6	AX012285	AX012285	Sequence
5	47.4	83.2	57	6	AX012286	AX012286	Sequence
6	47.4	83.2	57	6	AX012287	AX012287	Sequence
7	47.4	83.2	57	6	AX012288	AX012288	Sequence
8	47.4	83.2	57	6	AX012289	AX012289	Sequence
9	47.4	83.2	57	6	AX012290	AX012290	Sequence
10	34	59.6	37	6	AX012231	AX012231	Sequence
11	29.4	51.6	52	6	AR021007	AR021007	Sequence
12	29.4	51.6	52	6	AR021047	AR021047	Sequence
13	29.4	51.6	52	6	AR043422	AR043422	Sequence
14	29.4	51.6	52	6	AR043462	AR043462	Sequence
15	29.4	51.6	52	6	AR062337	AR062337	Sequence
16	29.4	51.6	52	6	AR062377	AR062377	Sequence
17	29.4	51.6	52	6	AR183796	AR183796	Sequence
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other sequences; artificial sequences.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
ANANVORANICH,S., Lafontaine,D. and Perreault,J.P.
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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RESULT 3
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LOCUS
DEFINITION
Sequence 45 from Patent WO9955856.
ACCESSION
AX012283
VERSION
AX012283.1 GI:9998344
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS
ANANVORANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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AX012285
VERSION
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ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVORANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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VERSION
AX012286.1 GI:9998347
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ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS
ANANVORANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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DEFINITION
Sequence 49 from Patent WO9955856.
ACCESSION
AX012287
VERSION
AX012287.1 GI:9998348
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVORANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 49 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J.
and Driver,D.A.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 5789245-A 40 04-AUG-1998;
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DEFINITION Sequence 80 from patent US 5814482.
ACCESSION AR043462
VERSION AR043462.1 GI:5964470
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 80 29-SEP-1998;
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DEFINITION Sequence 40 from patent US 5843723.
ACCESSION AR062337
VERSION AR062337.1 GI:5990028
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W.,
Jolly,D.J., Driver,D.A. and Belli,B.A.
TITLE Alphavirus vector constructs
JOURNAL Patent: US 5843723-A 40 01-DEC-1998;
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ACCESSION AR043422
VERSION AR043422.1 GI:5964430
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 40 29-SEP-1998;
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DEFINITION Sequence 80 from patent US 5789245.
ACCESSION AR021047
VERSION AR021047.1 GI:3975662
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J.
and Driver,D.A.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 5789245-A 80 04-AUG-1998;
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ACCESSION AR021047
VERSION AR021047.1 GI:3975662
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J.
and Driver,D.A.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 5789245-A 80 04-AUG-1998;
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DEFINITION Sequence 40 from patent US 5814482.
ACCESSION AR043422
VERSION AR043422.1 GI:5964430
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 40 29-SEP-1998;
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RESULT 14
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DEFINITION Sequence 80 from patent US 5814482.
ACCESSION AR043462
VERSION AR043462.1 GI:5964470
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 80 29-SEP-1998;
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Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
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DEFINITION Sequence 40 from patent US 5843723.
ACCESSION AR062337
VERSION AR062337.1 GI:5990028
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W.,
Jolly,D.J., Driver,D.A. and Belli,B.A.
TITLE Alphavirus vector constructs
JOURNAL Patent: US 5843723-A 40 01-DEC-1998;
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DEFINITION Sequence 40 from patent US 5814482.
ACCESSION AR043422
VERSION AR043422.1 GI:5964430
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 40 29-SEP-1998;
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Job time : 1125 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:06:47 ; Search time 868.86 Seconds
(without alignments)
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Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 6	16	80.0	257	1	AV027102
C 7	16	80.0	327	9	CE236428
C 8	16	80.0	512	1	AI481854
C 9	16	80.0	534	2	AW699095
C 10	16	80.0	557	4	BG023212
C 11	16	80.0	557	8	BZ261544
C 12	16	80.0	575	2	BF231936
C 13	16	80.0	751	5	BX847762
C 14	16	80.0	905	7	CN501110
C 15	16	80.0	971	9	CC995546
C 16	16	80.0	1165	8	BZ562536
C 17	15.8	79.0	254	9	CE795156
C 18	15.8	79.0	314	2	BB518409
C 19	15.8	79.0	358	7	N41730
C 20	15.8	79.0	370	7	CE806241
C 21	15.8	79.0	408	7	CR584508
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C 23	15.8	79.0	454	8	B60215
C 24	15.8	79.0	459	1	AI368409

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C 26	15.8	79.0	498	9	CL609413
C 27	15.8	79.0	519	8	BH090915
C 28	15.8	79.0	525	8	AQ545150
C 29	15.8	79.0	577	4	BM263519
C 30	15.8	79.0	578	5	BQ632754
C 31	15.8	79.0	617	7	CK824498
C 32	15.8	79.0	1104	8	CC262353
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C 37	15.6	78.0	529	1	AA930487
C 38	15.6	78.0	553	2	BE751983
C 39	15.6	78.0	589	7	CK428113
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ALIGNMENTS

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BB152189/c
LOCUS BB152189 RIKEN full-length enriched, 16 days neonate thymus Mus
DEFINITION musculus cDNA clone AL30004F20 3', mRNA sequence.
ACCESSION BB152189
VERSION BB152189.1 GI:8807126
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 226)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayateu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kigawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watanabe,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and thermoinactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitanai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
1..226
/organism="Mus musculus"
/mol_type="mrna"
/db_xref="taxon:10090"
/clone="A130004F20"
/tissue_type="thymus"
/dev_stage="16 days neonate"
/lab_host="DH108"
/clone_lib="RIKEN full-length enriched, 16 days neonate thymus"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCTCGATTAAATTAATTCCTCCCTCCCTCC sequence [5' GAGAGAGATCTCGATTAAATTAATTCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PUC I."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 226;
Best Local Similarity 70.0%; Pred. No. 8.8e+02;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGACCC 20
DB 54 CGGAATGCTAAGGACCC 35

RESULT 2

AZ844319/c
LOCUS 240 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0143C17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0143C17 R, genomic survey sequence.
ACCESSION AZ844319
VERSION AZ844319.1 GI:13014227
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 240)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0143 row: C column: 17

FEATURES

source
1..240
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0143C17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 240;
Best Local Similarity 70.0%; Pred. No. 8.9e+02;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGACCC 20
DB 121 GGGGATGGCTCAGGACCC 102

RESULT 3

AZ791672/c
LOCUS 514 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0041L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0041L08 R, genomic survey sequence.
ACCESSION AZ791672
VERSION AZ791672.1 GI:12934808
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 514)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0041 row: L column: 08

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 240.
Location/Qualifiers

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 514.

Location/Qualifiers

FEATURES

source

1. .514

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0041L08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (G1[4732114]gb/AP129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 514;
Best Local Similarity 70.0%; Pred. NO. 9.9e+02;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20

Db 322 GGGCATGCTCAGGACCC 303

RESULT 4

AI233177

LOCUS

DEFINITION EST229865 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone

AI233177

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

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AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

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AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

AI233177.1 GI:3817057

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AI233177.1 GI:3817057

AI233177.1 GI:3817057

/db_xref="ATCC (inhost):2040225"

/clone_lib="taxon:10118"

/clone_lib="RKICL81"

/note="Organ: kidney; Vector: pT73Pac; Site_1: EcoRI;

Site_2: NotI"

ORIGIN

Query Match 84.0%; Score 16.8; DB 1; Length 557;
Best Local Similarity 70.0%; Pred. NO. 1e+03;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20

Db 286 GGGCATGCTCAGGACCC 305

RESULT 5

BU361862

LOCUS

DEFINITION

603789355F1 CSEQCHN72 Gallus gallus cDNA clone

sequence.

ACCESSION

BU361862

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 916)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

2235534

12445392

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. 916

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="Compton Line 151"

/db_xref="taxon:9031"

/clone="ChEST750m14"

/sex="Female"

/tissue_type="cerebrum"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="CSEQCHN72"

/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:

EcoRI; Site_2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was blunted, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

FEATURES

source

1. .557

/organism="Rattus sp."

/mol_type="mRNA"

ORIGIN

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Query Match      82.0%; Score 16.4; DB 5; Length 916;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGAC 18
Db :|||:|||||
84 GGGGATGCTAAGGAC 101

RESULT 6
AV027102/c
LOCUS AV027102 Mus musculus adult C57BL/6J liver Mus musculus cDNA clone
DEFINITION 1300004P23, mRNA sequence.
ACCESSION AV027102
VERSION AV027102.1 GI:4806712
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 257)
Owaka, S., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y.,
Tomihata, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermotabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1..257
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="1300004P23"
/tissue_type="liver"
/dev_stage="adult"
/clone_lib="Mus musculus adult C57BL/6J liver"

ORIGIN
Query Match      80.0%; Score 16; DB 1; Length 257;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCGAUGGCUAAGGACCC 20
Db :|||:|||||
88 GGAATGGCTAAGGACCC 71

RESULT 7
CE236428/c
LOCUS CE236428 327 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-1700033390000 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE236428

Query Match      82.0%; Score 16.4; DB 5; Length 916;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGAC 18
Db :|||:|||||
84 GGGGATGCTAAGGAC 101

RESULT 6
AV027102/c
LOCUS AV027102 Mus musculus adult C57BL/6J liver Mus musculus cDNA clone
DEFINITION 1300004P23, mRNA sequence.
ACCESSION AV027102
VERSION AV027102.1 GI:4806712
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 257)
Owaka, S., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y.,
Tomihata, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermotabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1..257
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="1300004P23"
/tissue_type="liver"
/dev_stage="adult"
/clone_lib="Mus musculus adult C57BL/6J liver"

ORIGIN
Query Match      80.0%; Score 16; DB 1; Length 257;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCGAUGGCUAAGGACCC 20
Db :|||:|||||
88 GGAATGGCTAAGGACCC 71

RESULT 7
CE236428/c
LOCUS CE236428 327 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-1700033390000 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE236428

Query Match      82.0%; Score 16.4; DB 5; Length 916;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGAC 18
Db :|||:|||||
84 GGGGATGCTAAGGAC 101

RESULT 6
AV027102/c
LOCUS AV027102 Mus musculus adult C57BL/6J liver Mus musculus cDNA clone
DEFINITION 1300004P23, mRNA sequence.
ACCESSION AV027102
VERSION AV027102.1 GI:4806712
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 257)
Owaka, S., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y.,
Tomihata, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermotabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1..257
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1300004P23"
/tissue_type="liver"
/dev_stage="adult"
/clone_lib="Mus musculus adult C57BL/6J liver"

ORIGIN
Query Match      80.0%; Score 16; DB 1; Length 257;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCGAUGGCUAAGGACCC 20
Db :|||:|||||
88 GGAATGGCTAAGGACCC 71

RESULT 7
CE236428/c
LOCUS CE236428 327 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-1700033390000 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE236428

Query Match      82.0%; Score 16.4; DB 5; Length 916;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGAC 18
Db :|||:|||||
84 GGGGATGCTAAGGAC 101

RESULT 6
AV027102/c
LOCUS AV027102 Mus musculus adult C57BL/6J liver Mus musculus cDNA clone
DEFINITION 1300004P23, mRNA sequence.
ACCESSION AV027102
VERSION AV027102.1 GI:4806712
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 257)
Owaka, S., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y.,
Tomihata, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermotabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1..257
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1300004P23"
/tissue_type="liver"
/dev_stage="adult"
/clone_lib="Mus musculus adult C57BL/6J liver"

ORIGIN
Query Match      80.0%; Score 16; DB 1; Length 257;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCGAUGGCUAAGGACCC 20
Db :|||:|||||
159 GGCATGGCTGAGGGACCC 142

RESULT 8
AI481854
LOCUS AI481854 512 bp mRNA linear EST 09-MAR-1999
DEFINITION vj74dl1.xi Knowles Solter mouse blasocyst B1 Mus musculus cDNA
clone IMAGE:934773 3' similar to SW:DHAX_HUMAN P49419 ANTIQUITIN ;,
mRNA sequence.
ACCESSION AI481854
VERSION AI481854.1 GI:4375080
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 512)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:539693
This clone was previously sequenced on the 5' end only, this new

```

```

data is from the 3' end
Possible reversed clone: similarity on wrong strand
Seq primer: Primer name ambiguous
High quality sequence stop: 77.
Location/Qualifiers
1..512
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:934773"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
/clone_lib="Knuckles Solter mouse blastocyst B1"
/notes="Organ: embryo; Vector: pSPORT; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: SalI (df) :
5'-CGGTGCACGTGCACGGTATTTTTTTT-3'. cDNAs were
cloned into the NotI/SalI sites of a pSPORT vector (Life
Technologies). Two different size selections: B1 (larger
inserts) and B3."

```

```

ORIGIN
      80.0%;   Score 16;   DB 1;   Length 512;
Query Match      77.8%;   Pred.No. 2.5e+03;
Best Local Similarity
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      3  SGCAUGGCUAAGGACCC 20
      :|:|:|:|:|:|:|:|:|
Db      214  GGAATGCTAAGGACCC 231

```

RESULT	9
LOCUS	AW699095
DEFINITION	534 bp mRNA linear EST 18-APR-2000 P20G03.Y1 Moss EST library PPN Physcomitrella patens cDNA clone PEB SOURCE_ID:PPN11205 5', mRNA sequence.
ACCESSION	AW699095
VERSION	AW699095.1 GI:7582931
KEYWORDS	EST.
SOURCE	Physcomitrella patens
ORGANISM	Physcomitrella patens
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Erysoida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 534)
AUTHORS	Quatrano,R., Bashardes,S., Cove,D., Cuming,A., Knight,C., Clifton,S., Marra,M., Hillier,L., Fape,D., Martin,J.J., Wylie,T., Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Steptoe,M., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
TITLE	Leeds/Wash U Moss EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Ralph Quatrano Leeds/Wash U Moss EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810

```
FEATURES
source
1. .534
/organism="Physcomitrella patens"
/mol_type="mRNA"
/db_xref="taxon:3218"
/clone="PEP SOURCE ID:PPN111205"
magn quality sequence stop: 417.
Location/Qualifiers
```

/tissue_types="protonemata: 7 day old tissue auxin treated
/lab host="DH10B"
/clone lib="Moss EST library PPN"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Construction of the cDNA library was carried out
using Strategenes 'Unizap - cDNA synthesis kit'. cDNA was
constructed using an oligo dt primer/linker that contains
a XhoI site within it. Following ds cDNA synthesis,
EcoRI adapters were ligated to the blunt ends and sample
was digested with XhoI. The result is cDNA with an EcoRI
sticky end on one side and a XhoI sticky end on the other.
This cDNA was ligated directionally in Unizap arms. The
vector is designed containing the pBluescript sequence as
well as lambda DNA and cDNA is cloned within this
pBluescript sequence. The vector was then packaged using
Gold gigapackaging extracts. Library was grown in XLBlue
MR⁺ cells and amplified. The library was excised by mass
excision using Strategenes 'Mass excision kit' that uses
exassist as a helper phage that releases the pBluescript
sequence and circularises it as single stranded plasmids
that are then packaged (by helper phage) and secreted out
of the host cell as phagemids. SOLR cells were transformed
with phagemids and the library was plated out on LB-amp
plates to select for transformants. Approximately
1,000,000 colonies were grown and recovered. The double
stranded plasmid library was recovered by using Qiagen
Midi prep kit. 2 micro grams of each library were used to
transform DH10B cells by electroporation."

ORIGIN	
Query Match	80.0%; Score 16; DB 2; Length 534;
Best Local Similarity	83.3%; Pred. NO. 2.5e+03;
Matches 15; Conservative	2; Mismatches 1; Indels 0; Gaps 0;
Qy	3 SGCAUGGCUAAGGGACCC 20
	: :
Db	123 GGCATGGCAAAGGGACCC 140

RESULT 10
 BG023212
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BG023212
 df10c01.y1 Wellcome CRC PRN3 S13 17 egg animal cap Xenopus laevis
 cDNA clone IMAGE:3556968 5', mRNA sequence.
 557 bp mRNA linear EST 24-JAN-2001
 BG023212.1 GI:12479291
 EST.
 Xenopus laevis
 Xenopus laevis
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 557)
 Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
 Pape,D., Martin,J., Wylie,I., Underwood,K., Theising,B., Bowers,Y.,
 Person,B., Gibbons,M., Hurvey,N., Ritter,E., Jackson,Y., McCann,R.,
 Waterston,R. and Wilson.R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 Other ESTs: df10c01.x1

Other_ESTs: df10c01.xl
Contact: Sandy Clifton, Ph.D.
Wasnu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by N. Garrett, E. Ellefroid, and A.M. Zorn
(Wellcome/CRC Institute). DNA Sequencing by: Washington University
Genome Sequencing Center
Clone Distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seg primer: -40RP from Gibco

FEATURES source
High quality sequence stop: 519.
Location/Qualifiers
1..557

/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3556968"
/tissue_type="egg, subtracted by stage 13-17 animal cap"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC pRN3 St13 17 egg animal cap"
/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett, E. Bellefroid, and A.M. Zorn, (Wellcome/CRC Institute)."

ORIGIN

Query Match 80.0%; Score 16; DB 4; Length 557;
Best Local Similarity 77.8%; Pred. No. 2.6e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 SGCAUGGCUAAGGACCC 20
Db 486 CGCATGGCTAAGGACCC 503
:||||:|||||

RESULT 11

BZ261544/c
LOCUS BZ261544.1 557 bp DNA linear GSS 15-OCT-2002
DEFINITION CH230-458G21.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-458G21, genomic survey sequence.

ACCESSION BZ261544

VERSION BZ261544.1

KEYWORDS GSS.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 557)

Authors: Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.

Title: Rat BAC End Sequences from Library CHORI-230 MboI segment

Journal: Unpublished (1999)

Comment: Other GSSs: CH230-458G21.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rat230.htm>). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(<http://www.chori.org/bacpac/orering.information.htm>). BAC end

plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Seq primer: SP6

Class: BAC ends.

FEATURES

source
Location/Qualifiers
1..557
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-458G21"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;

CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Query Match 80.0%; Score 16; DB 8; Length 557;
Best Local Similarity 77.8%; Pred. No. 2.6e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 SGCAUGGCUAAGGACCC 20
Db 23 GGCATGGCTAAGTACCC 6
:||||:|||||

RESULT 12

LOCUS BF231936/c 575 bp mRNA linear EST 11-DEC-2000
DEFINITION df10c01.x1 Wellcome CRC pRN3 St13 17 egg animal cap Xenopus laevis
CDNA clone IMAGE:3556968 3', mRNA sequence.

ACCESSION BF231936

VERSION BF231936.1

KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 575)

Authors: Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L.,

Pape, D., Martin, J., Wylie, F., Underwood, K., Theising, B., Bowers, Y.,

Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,

Waterston, R., and Wilson, R.

Title: Washu Xenopus EST project, 1999

Journal: Unpublished (1999)

Comment: Contact: Sandy Clifton, Ph.D.

Washu Xenopus EST project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by N. Garrett, E. ellefroid, and A.M. Zorn

(Wellcome/CRC Institute). DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

High quality sequence stop: 494.

Location/Qualifiers

1..575

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:3556968"

/tissue_type="egg, subtracted by stage 13-17 animal cap"

/lab_host="DH10B (phage-resistant)"

/clone_lib="Wellcome CRC pRN3 St13 17 egg animal cap"

/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs

were oligo-dT primed and directionally cloned. Staging

according to Nieuwkoop and Faber. Library is subtracted

and was constructed by N. Garrett, E. Bellefroid, and A.M.

Zorn, (Wellcome/CRC Institute)."

ORIGIN

Query Match 80.0%; Score 16; DB 2; Length 575;
Best Local Similarity 77.8%; Pred. No. 2.6e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 SGCAUGGCUAAGGACCC 20
Db 555 CGCATGGCTAAGGACCC 538
:||||:|||||

RESULT 13

BX847762

LOCUS BX847762 751 bp mRNA linear EST 11-DEC-2003
DEFINITION BX847762 Wellcome CRC pR3 St13 17 egg animal cap xenopus laevis
ACCESSION CDNA clone IMAGE998E018659 ; IMAGE:3556968 5', mRNA sequence.
VERSION BX847762
KEYWORDS BX847762.1 GI:39736970
SOURCE EST.
ORGANISM Xenopus laevis (African clawed frog)

REFERENCE
AUTHORS Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 751)
 Heil, O., Neubert, P., Peters, M., Radelof, U., Schneider, D.,
 Schroth, A., Korn, B. and Landgrebe, J.
 Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
 Unpublished (2003)
TITLE Contact: Ina Rolfs
JOURNAL RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
COMMENT Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE998E018659.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB
 No.988) http://www.rzpd.de/cgi-
 bin/products/showLib.pl.cgi?responderlibNo=998 RZPDLIB; Xenopus
 laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
 bin/products/showLib.pl.cgi?responderlibNo=988 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 RN_f, 5' CGAGAAGCTCAGATAAAGCTC 3'.

FEATURES
 source
 1..751
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:3556968"
 /tissue_type="egg, subtracted by stage 13-17 animal cap"
 /lab_host="PH108 (phage-resistant)"
 /clone_lib="Wellcome CRC pR3 St13 17 egg animal cap"
 /note="Vector: pSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Staging
 according to Nieuwkoop and Faber. Library is subtracted
 and was constructed by N. Garrett, E Bellefroid, and A.M.
 Zorn, (Wellcome/CRC Institute)."
 ORIGIN
 Query Match 80.0%; Score 16; DB 5; Length 751;
 Best Local Similarity 77.8%; Pred. No. 2.7e+03;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SCGAUGGCUAGGACCC 20
 :|||:|||||
 Db 503 CGCATGGCTAGGACCC 520

RESULT 14
LOCUS CN501110/c
DEFINITION AGENCOURT 22405065 NIH_ZGC_9 Danio rerio CDNA clone IMAGE:7273520
 5', mRNA sequence.
ACCESSION CN501110
VERSION CN501110.1 GI:46813734
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 905)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Chi-Bin Chien
 cDNA Library Preparation: Dr. Sumio Sugano
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM15261 row: a column: 06
 High quality sequence start: 8
 High quality sequence stop: 718.

FEATURES
 source
 1..905
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7273520"
 /tissue_type="neural retina, retinal pigment epithelium,
 lens and overlying skin, pooled embryos"
 /lab_host="DH10B Tona"
 /clone_lib="NIH ZGC 9"
 /note="Organ: eye; Vector: pME18S-FL3; Site 1: DraIII;
 Site 2: DraIII; 1st strand cDNA was primed with an
 oligo(dT) primer
 [CGGCTGAAGACGCCCTATGGCTTTTCTTTTCTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [GGCCUACUGG], digested and directionally cloned into
 distinct DraIII sites of the pME18S-FL3. Library was size
 selected for 1.0 kb, with a average insert size of ~1.2kb,
 and is not amplified. Library constructed by Yutaka Suzuki
 (University of Tokyo Institute of Medical Science). Custom
 primers recommended for sequencing: 5' end primer
 5'-GGATGTGCTTACTTCTA-3' and 3' end primer
 5'-CGACCTCGAGCTCGACACA-3'. Note: This is a Zebrafish Gene
 Collection (ZGC) library"
 ORIGIN
 Query Match 80.0%; Score 16; DB 7; Length 905;
 Best Local Similarity 77.8%; Pred. No. 2.7e+03;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SCGAUGGCUAGGACCC 20
 :|||:|||||
 Db 730 CGCTGGCTAGGACCC 713

RESULT 15
LOCUS CC995546
DEFINITION ZUAH125TV 2M 3.0 4.0 KB Zea mays genomic clone ZMMBPA0069F01,
 genomic survey sequence.
ACCESSION CC995546
VERSION CC995546.1 GI:33855422
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 971)
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other_GSSs: ZUAH125TH
 Contact: Cathy Whitelaw

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteaw@tigr.org
Seq primer: TF
Class: sheared ends.

```

FEATURES
    source
        Location/Qualifiers
            1..971
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMMBPa0069F01"
                /clone_lib="ZM_3-0_4.0 KB"
                /note="vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
                genomic DNA library"

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ORIGIN

Query Match 80.0%; Score 16; DB 9; Length 971;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGCAUGGCUAAGGACCC 20
 :|||:|||:|||:|||
Db 660 CGCATGGCTAAGGAACCC 677

Search completed: March 15, 2005, 15:20:45
Job time : 873.86 secs


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Query Match      82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGNNNNNNNUGGCAUCCG 35
    :|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGGTCCGACCTGGCATCCG 32

RESULT 13
US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,140A
; FILING DATE: 22-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cullman, Louis C.
; REGISTRATION NUMBER: 39,645
; REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 823.6000
; TELEFAX: (949) 823.6100
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match      82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGNNNNNNNUGGCAUCCG 35
    :|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGGTCCGACCTGGCATCCG 32

RESULT 15
US-09-415-784-39
; Sequence 39, Application US/09415784
; Patent No. 6391632
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Prolov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-415-784-39

Query Match 78.4%; Score 29; DB 3; Length 56;
Best Local Similarity 58.6%; Pred. No. 13;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGNNNNNUGGCAU 32
Db 27 TCACCTCTCGCGGTCGACCTGGGCAT 55

Search completed: March 15, 2005, 20:44:22
Job time : 61.5044 secs

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Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNNUGGCAUGC 34
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 13

US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236

GENERAL INFORMATION:

APPLICANT: Dubensky Jr., Thomas W

Polo, John M.

Ibanez, Carlos E.

Chang, Stephen M.W.

Jolly, Douglas J.

Driver, David A.

Belli, Barbara A.

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY

STREET: 840 NEWPORT CENTER DRIVE, SUITE 700

CITY: NEWPORT BEACH

STATE: CALIFORNIA

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/236,140A

APPLICATION NUMBER: US/09/236,140A

FILING DATE: 22-Jan-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Cullman, Louis C.

REGISTRATION NUMBER: 39,645

REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (949) 823.6000

TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-236-140A-40

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNNUGGCAUGC 34
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 14

US-09-236-140A-80

; Sequence 80, Application US/09236140A

; Patent No. 6376236

GENERAL INFORMATION:

APPLICANT: Dubensky Jr., Thomas W

Polo, John M.

Ibanez, Carlos E.

Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/236,140A

APPLICATION NUMBER: US/09/236,140A

FILING DATE: 22-Jan-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Cullman, Louis C.

REGISTRATION NUMBER: 39,645

REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (949) 823.6000

TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 80:

US-09-236-140A-80

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNNUGGCAUGC 34
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 15

US-09-415-784-39

; Sequence 39, Application US/09415784

; Patent No. 6391632

GENERAL INFORMATION:

APPLICANT: Dubensky Jr., Thomas W.

Polo, John M.

Belli, Barbara A.

Schlesinger, Sondra

Dryga, Sergey A.

Prolov, Ilva

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
SYNTHESIS

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group PLLC

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC-compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-415-784-39

Query Match 50.9%; Score 29; DB 3; Length 56;
Best Local Similarity 58.6%; Pred. No. 60;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UCCACCCUCCGCGGNNNNNNNUGGCGAU 32
Db 27 TCCACCTCCGCGTCCGACCTGGGCAT 55

Search completed: March 15, 2005, 20:44:22
Job time : 95.75 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:59:13 ; Search time 132.105 Seconds
(without alignments)
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Title: US-09-699-667E-66

Perfect score: 20

Sequence: 1 bksgaugcuaaggagacc 20

Scoring table:

IDENTITY_NUCDX

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Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.8	84.0	98146	18	US-10-322-281-126
2	16	80.0	25	19	US-10-719-900-844389
3	15.8	79.0	552	13	US-10-027-632-281354
4	15.8	79.0	552	17	US-10-027-632-281354
5	15.8	79.0	772	9	US-09-764-877-2608
6	15.8	79.0	772	17	US-10-242-515-2608
7	15.8	79.0	1010	18	US-10-437-963-77165
8	15.8	79.0	191597	18	US-10-719-993-6802
9	15.6	78.0	201	18	US-10-719-993-53406
10	15.6	78.0	358	18	US-10-425-115-115288
11	15.6	78.0	98686	17	US-10-189-267-20

C	12	15.6	78.0	115434	18	US-10-719-993-7058	Sequence 7058, Ap
	13	15.4	77.0	353	9	US-09-960-352-9080	Sequence 9080, Ap
	14	15.4	77.0	442	17	US-10-424-599-53225	Sequence 53225, A
C	15	15.4	77.0	454	9	US-09-864-761-1027	Sequence 1027, Ap
C	16	15.4	77.0	459	13	US-10-027-632-56559	Sequence 56559, A
C	17	15.4	77.0	459	17	US-10-027-632-56559	Sequence 56559, A
C	18	15.4	77.0	483	13	US-10-027-632-3457	Sequence 3457, Ap
	19	15.4	77.0	483	17	US-10-027-632-3457	Sequence 3457, Ap
C	20	15.4	77.0	622	13	US-10-027-632-189843	Sequence 189843, A
C	21	15.4	77.0	622	13	US-10-027-632-189843	Sequence 189843, A
C	22	15.4	77.0	622	17	US-10-027-632-189843	Sequence 189843, A
C	23	15.4	77.0	622	17	US-10-027-632-189843	Sequence 189843, A
C	24	15.4	77.0	822	18	US-10-437-963-18371	Sequence 18371, A
	25	15.4	77.0	20190	10	US-09-996-015-3	Sequence 3, Appli
	26	15.4	77.0	20190	17	US-10-287-190-167	Sequence 167, App
	27	15.4	77.0	20190	17	US-10-307-817-153	Sequence 153, App
C	28	15.4	77.0	57130	9	US-09-835-081-3	Sequence 3, Appli
C	29	15.4	77.0	135005	18	US-10-723-860-2320	Sequence 2320, Ap
C	30	15.2	76.0	201	19	US-10-741-600-45160	Sequence 45160, A
C	31	15.2	76.0	273	18	US-10-723-860-3342	Sequence 3342, Ap
C	32	15.2	76.0	479	10	US-09-918-995-338	Sequence 338, App
C	33	15.2	76.0	487	13	US-10-027-632-63615	Sequence 63615, A
C	34	15.2	76.0	487	13	US-10-027-632-107839	Sequence 107839, A
C	35	15.2	76.0	487	17	US-10-027-632-63615	Sequence 63615, A
C	36	15.2	76.0	487	17	US-10-027-632-107839	Sequence 107839, A
C	37	15.2	76.0	572	13	US-10-027-632-231346	Sequence 231346, A
C	38	15.2	76.0	572	13	US-10-027-632-231346	Sequence 231346, A
C	39	15.2	76.0	612	13	US-10-027-632-189769	Sequence 189769, A
	40	15.2	76.0	612	13	US-10-027-632-189770	Sequence 189770, A
	41	15.2	76.0	612	13	US-10-027-632-189771	Sequence 189771, A
	42	15.2	76.0	612	17	US-10-027-632-189769	Sequence 189769, A
	43	15.2	76.0	612	17	US-10-027-632-189770	Sequence 189770, A
	44	15.2	76.0	612	17	US-10-027-632-189771	Sequence 189771, A
C	45	15.2	76.0	621	13	US-10-027-632-227686	Sequence 227686, A

ALIGNMENTS

RESULT 1
US-10-322-281-126
; Sequence 126, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 98146
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(98146)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-126

Query Match	84.0%	Score 16.8;	DB 18;	Length 98146;
Best Local Similarity	70.0%	Pred. No. 52;		
Matches 14;	Conservative 5;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	BKSGAUGCUAAGGAGACC 20		
Db	46153	CTGGCATGCTAAGGACAC 46172		
RESULT 2				
US-10-719-900-844389				

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; Sequence 844389, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Wei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-844389

Query Match      80.0%; Score 16; DB 19; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db   5  GCATGGCTAAGGACC 20
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RESULT 3
US-10-027-632-281354/c
; Sequence 281354, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281354
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281354

Query Match      79.0%; Score 15.8; DB 17; Length 552;
Best Local Similarity 68.4%; Pred. No. 2.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY  1  BKSGCAUGGCUAAGGACC 19
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Db   406  TTGGCATGGCTAAAGGACC 388
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RESULT 5
US-09-764-877-2608/c
; Sequence 2608, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2608
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2608

Query Match      79.0%; Score 15.8; DB 9; Length 772;
Best Local Similarity 68.4%; Pred. No. 2.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY  1  BKSGCAUGGCUAAGGACC 19
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Db   84  TTGGCATGGCTAAGGACC 66
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RESULT 6
US-10-242-515-2608/c
; Sequence 2608, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2608
LENGTH: 772
TYPE: DNA
ORGANISM: Homo sapiens
US-10-242-515-2608

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 17; Length 772;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19
DB 84 TTGGCATGGCTAAGGTC 66

RESULT 7
US-10-437-963-77165/c
Sequence 77165, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
Plants of Invention: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 77165
LENGTH: 1010
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1010)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_7708C.1
US-10-437-963-77165

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 18; Length 1010;

Best Local Similarity 73.7%; Pred. No. 2.1e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19
DB 67 TGGGCAGGCTAAGGACC 49

RESULT 8
US-10-719-993-6802
Sequence 6802, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6802
LENGTH: 191597
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-6802

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 18; Length 191597;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19
DB 50713 CTGGCATGGCTAAGGACC 50731

RESULT 9
US-10-719-993-53406/c
Sequence 53406, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53406
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-53406

Query Match
Best Local Similarity 78.0%; Score 15.6; DB 18; Length 201;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 20
DB 189 TGTGCATGGCTAAGGACTC 170

RESULT 10
US-10-425-115-115288
Sequence 115288, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 115288
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_36627C.1
US-10-425-115-115288

Query Match 78.0%; Score 15.6; DB 18; Length 358;
Best Local Similarity 72.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGACC 19
DB 229 GGGGATGCTAAGGACC 246
:::|||||

RESULT 11
US-10-189-267-20
; Sequence 20, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 20
; LENGTH: 98686
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 28031, 59631, 59767, 78835-78934, 96078-96177
; OTHER INFORMATION: n = A,T,C or G
US-10-189-267-20

Query Match 78.0%; Score 15.6; DB 17; Length 98686;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 20
DB 68874 CTAGCATGGCAAAGGACC 68893
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RESULT 12
US-10-719-993-7058/c
; Sequence 7058, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7058
; LENGTH: 115434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-7058

Query Match 78.0%; Score 15.6; DB 18; Length 115434;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 20
DB 93388 TGTGCATGGCTAAGGACTC 93369
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RESULT 13
US-09-960-352-9080
; Sequence 9080, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9080
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (271)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 39-LIB3058-011-Q1-K1-B4
US-09-960-352-9080

Query Match 77.0%; Score 15.4; DB 9; Length 353;
Best Local Similarity 82.4%; Pred. No. 3.6e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 20
DB 208 GCATGGCTGAGGACC 224
:::|||||

RESULT 14
US-10-424-599-53225
; Sequence 53225, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 53225
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19074C.1
US-10-424-599-53225

Query Match 77.0%; Score 15.4; DB 17; Length 442;
Best Local Similarity 82.4%; Pred. No. 3.6e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 20

Db 232 GCATGGCTATGGGACCC 248
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RESULT 15
US-09-864-761-1027/c
; Sequence 1027, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864, 761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1027
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009228.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
US-09-864-761-1027

Query Match 77.0%; Score 15.4; DB 9; Length 454;
Best Local Similarity 70.6%; Pred. NO. 3.6e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGGA 17
Db 435 CTGGCATGGCTAAGGGA 419
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Job time : 134.105 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:26:58 ; Search time 94.75 Seconds
(without alignments)
984.356 Million cell updates/sec

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Perfect score: 57
Sequence: 1 ggguccaccuccgcggun.....cgggcauggcuaagggaccc 57

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29.4	51.6	52	1	US-08-741-881-40 Sequence 40, Appl
2	29.4	51.6	52	1	US-08-741-881-80 Sequence 80, Appl
3	29.4	51.6	52	1	US-08-739-158-40 Sequence 40, Appl
4	29.4	51.6	52	1	US-08-739-158-80 Sequence 80, Appl
5	29.4	51.6	52	2	US-08-739-167-40 Sequence 40, Appl
6	29.4	51.6	52	2	US-08-739-167-80 Sequence 80, Appl
7	29.4	51.6	52	3	US-08-404-796-40 Sequence 40, Appl
8	29.4	51.6	52	3	US-08-404-796-80 Sequence 80, Appl
9	29.4	51.6	52	3	US-08-931-869-40 Sequence 40, Appl
10	29.4	51.6	52	3	US-08-931-869-80 Sequence 80, Appl
11	29.4	51.6	52	3	US-09-350-399-40 Sequence 40, Appl
12	29.4	51.6	52	3	US-09-350-399-80 Sequence 80, Appl
13	29.4	51.6	52	3	US-09-236-140A-40 Sequence 40, Appl
14	29.4	51.6	52	3	US-09-236-140A-80 Sequence 80, Appl
15	29.4	50.9	56	3	US-09-415-784-39 Sequence 39, Appl
16	29.4	50.9	56	3	US-09-415-785A-39 Sequence 39, Appl
17	29.4	50.9	56	3	US-08-944-465-39 Sequence 39, Appl
18	29.4	50.9	56	3	US-09-415-868-39 Sequence 39, Appl
19	29.4	50.9	56	3	US-09-415-900-39 Sequence 39, Appl
20	29.4	50.9	56	4	US-09-507-362-39 Sequence 39, Appl
21	24	42.1	52	1	US-08-238-963A-19 Sequence 19, Appl
22	23.2	40.7	47	4	US-09-422-978-3088 Sequence 3088, Ap
23	23	40.4	58	3	US-08-646-695-40 Sequence 40, Appl
24	23	40.4	58	5	PCT-US96-06053-40 Sequence 40, Appl
25	22.4	39.3	39	3	US-08-485-355B-7 Sequence 7, Appl
26	22.4	39.3	54	2	US-08-585-684B-2703 Sequence 2703, Ap
27	22.4	39.3	54	3	US-09-038-073-2703 Sequence 2703, Ap

28	22	38.6	45	2	US-08-632-882-5	Sequence 5, Appli
29	22	38.6	45	4	US-09-419-125-5	Sequence 5, Appli
30	22	38.6	49	1	US-08-758-306-6	Sequence 6, Appli
31	22	38.6	49	3	US-08-985-162-1875	Sequence 1875, Ap
32	22	38.6	49	3	US-08-998-099-373	Sequence 373, App
33	22	38.6	49	3	US-09-112-086B-7	Sequence 7, Appli
34	22	38.6	49	3	US-08-575-238-5	Sequence 5, Appli
35	22	38.6	49	3	US-09-094-381C-18	Sequence 18, Appl
36	22	38.6	49	3	US-08-679-645-1234	Sequence 1234, Ap
37	22	38.6	49	3	US-09-676-807-9	Sequence 9, Appli
38	22	38.6	49	4	US-09-216-584-38	Sequence 38, Appli
39	22	38.6	49	4	US-09-812-186-5	Sequence 5, Appli
40	22	38.6	49	4	US-09-401-063-1875	Sequence 1875, Ap
C 41	22	38.6	54	3	US-08-679-645-606	Sequence 606, App
C 42	21.8	38.2	38	4	US-09-474-432B-1309	Sequence 1309, Ap
C 43	21.8	38.2	38	4	US-09-476-387-1308	Sequence 1308, Ap
C 44	21.8	38.2	51	4	US-09-443-199C-881	Sequence 881, App
C 45	21.8	38.2	54	1	US-08-363-240A-1037	Sequence 1037, Ap

ALIGNMENTS

RESULT 1
US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

Query Match 51.6%; Score 29.4; DB 1; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNUGGCAUGC 34

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Db      1  TCCACCTCTCGGGTCCGACCTGGGCATCC 31
          :|||||:|||||:|||||:|||||:|||||:
RESULT 2
US-08-741-881-80
; Sequence 80, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-80
Query Match          51.6%; Score 29.4; DB 1; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4  UCCACCUCUCGCGGNNNNNUGGCAUGC 34
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Db      1  TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 3
US-08-739-158-40
; Sequence 40, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-739-158-40
Query Match          51.6%; Score 29.4; DB 1; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4  UCCACCUCUCGCGGNNNNNUGGCAUGC 34
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Db      1  TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 4
US-08-739-158-80
; Sequence 80, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-739-158-80
Query Match          51.6%; Score 29.4; DB 1; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4  UCCACCUCUCGCGGNNNNNUGGCAUGC 34
          :|||||:|||||:|||||:|||||:|||||:
Db      1  TCCACCTCTCGGGTCCGACCTGGGCATCC 31
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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80

Query Match          51.6%; Score 29.4; DB 1; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNUGGCAUGC 34
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 5
US-08-739-167-40
; Sequence 40, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-40

Query Match          51.6%; Score 29.4; DB 2; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNUGGCAUGC 34
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 6
US-08-739-167-80
; Sequence 80, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
;
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-80

Query Match          51.6%; Score 29.4; DB 2; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNUGGCAUGC 34
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCC 31

RESULT 7
US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-40

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCAUGC 34
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 8
US-08-404-796-80
Sequence 80, Application US/08404796
Patent No. 6015686
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-404-796-80

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCAUGC 34
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 9
US-08-931-869-40
Sequence 40, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 15-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-40

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCAUGC 34
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 10
US-08-931-869-80
Sequence 80, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:

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; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-931-869-80

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 34
Db 1 TCCACCTCTCGCGGTCGCGACCTGGGCATCC 31

RESULT 11
US-09-350-399-40
; Sequence 40, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; DRIVER, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
; US-09-350-399-40

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 34
Db 1 TCCACCTCTCGCGGTCGCGACCTGGGCATCC 31

RESULT 12
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; DRIVER, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
; US-09-350-399-80
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Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGCAUGC 34
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 13

US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,140A
; FILING DATE: 22-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cullman, Louis C.
; REGISTRATION NUMBER: 39,645
; REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 823.6000
; TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-236-140A-40

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGCAUGC 34
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 14

US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.

Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,140A
; FILING DATE: 22-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cullman, Louis C.
; REGISTRATION NUMBER: 39,645
; REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 823.6000
; TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match 51.6%; Score 29.4; DB 3; Length 52;
Best Local Similarity 58.1%; Pred. No. 44;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGCAUGC 34
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 15

US-09-415-784-39
; Sequence 39, Application US/09415784
; Patent No. 6391632
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilva

; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-415-784-39

Query Match 50.9%; Score 29; DB 3; Length 56;
Best Local Similarity 58.6%; Pred. No. 60;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAU 32
Db 27 TCCACCTCCTCGCGGTCCGACCTGGCAT 55

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Job time : 95.75 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-699-667E-62
Perfect score: 57
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	29.6	51.9	51	AAQ86173	Primer HD
6	29.4	51.6	48	ADR47040	Dengue vi
7	29.4	51.6	48	ADR48965	PCR prime
8	29.4	51.6	52	AQ86204	Sindbis/H
9	29.4	51.6	52	AAT31151	HDV rever
10	29.4	51.6	52	AAT30817	HDV riboz
11	29.4	51.6	52	AAV42394	Nested PC
12	29.4	51.6	52	AAV42426	Forward P
13	29.4	51.6	52	AAV60154	Nested PC
14	29.4	51.6	52	AAV60185	Reverse P
15	29.4	51.6	52	AAV70746	Reverse P
16	29.4	51.6	52	AAV70714	Nested pr
17	29.4	51.6	52	AAZ92930	Hepatitis
18	29.4	51.6	52	AAZ92970	Hepatitis
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21	29.4	51.6	52	6	AAZ57638	standard; RNA; 57 BP.
22	29.4	51.6	52	6	AAZ57638	
23	29.4	51.6	52	6	AAZ57638	
24	29.4	51.6	52	6	AAZ57638	
25	29.4	51.6	52	12	ADI30383	Hepatitis
26	29.4	51.6	52	12	ADI30423	Hepatitis
27	29.4	51.6	52	12	ADI30423	Hepatitis
28	29.4	51.6	52	12	ADI30423	Hepatitis
29	29.4	51.6	52	12	ADI30423	Hepatitis
30	29.4	51.6	52	12	ADI30423	Hepatitis
31	29.4	51.6	52	12	ADI30423	Hepatitis
32	29.4	51.6	52	12	ADI30423	Hepatitis
33	29.4	51.6	52	12	ADI30423	Hepatitis
34	29.4	51.6	52	12	ADI30423	Hepatitis
35	29.4	51.6	52	12	ADI30423	Hepatitis
36	29.4	51.6	52	12	ADI30423	Hepatitis
37	29.4	51.6	52	12	ADI30423	Hepatitis
38	29.4	51.6	52	12	ADI30423	Hepatitis
39	29.4	51.6	52	12	ADI30423	Hepatitis
40	29.4	51.6	52	12	ADI30423	Hepatitis
41	29.4	51.6	52	12	ADI30423	Hepatitis
42	29.4	51.6	52	12	ADI30423	Hepatitis
43	29.4	51.6	52	12	ADI30423	Hepatitis
44	29.4	51.6	52	12	ADI30423	Hepatitis
45	29.4	51.6	52	12	ADI30423	Hepatitis

ALIGNMENTS

RESULT 1	
AAZ57638	
ID AAZ57638 standard; RNA; 57 BP.	
XX	
AC AAZ57638;	
XX	
DT 15-SEP-2003 (revised)	
DT 05-APR-2000 (first entry)	
XX	
DE Trans-acting antigenomic delta ribozyme nucleotide sequence.	
XX	
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;	
KW inherited disease; ss.	
XX	
OS Hepatitis D virus.	
XX	
FH Key	Location/Qualifiers
FT misc_binding	1..6
FT	/tag= a
FT	/notes= "Forms double stranded region with bases 52-57"
FT	stem_loop
FT	7..19
FT	/tag= b
FT	misc_binding
FT	20..25
FT	/tag= c
FT	/bound_moiety= "SP1.1 substrate bases (AAZ57641) 5-11"
FT	stem_loop
FT	30..45
FT	/tag= d
FT	misc_binding
FT	52..57
FT	/tag= e
FT	/notes= "Forms a double stranded region with bases 6-1"
XX	
WO9955856-A2.	
PN	
XX	
PD 04-NOV-1999.	
XX	
PF 29-APR-1999;	99WO-CA000391.
XX	
PR 29-APR-1998;	98CA-02230203.
XX	
PA (UYSH) UNIV SHERBROOKE.	
XX	
PI Perreault J, Ananvoranich S, Lafontaine D;	
XX	

DR WPI; 2000-096791/08.
 XX New construction of nucleic acid enzyme useful for biotechnological,
 PT diagnostic and therapeutic applications.
 XX Example 1; Fig 2; 52pp; English.
 XX This is the nucleotide sequence of a trans-acting antigenomic delta
 CC ribozyme of the invention. This ribozyme cleaves substrate SP1.1 (see
 CC AA257641). The invention relates to a nucleic acid enzyme (e.g.
 CC deltaRzP1.1) that is constructed to have a substrate binding portion with
 CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
 CC sequence 5'-H*GNNHN-3'. The binding portion of the enzyme (ribozyme)
 CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
 CC (cleavage site is represented by *). At least one nucleotide is present
 CC 5' to the cleavage site of the substrate sequence. The enzyme of the
 CC invention is used to cleave a substrate nucleotide sequence at a specific
 CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
 CC to cleave viral RNA or RNA causing for example an inherited disease. The
 CC enzymes also have other therapeutic, biotechnological and diagnostic
 CC applications. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
 Query Match 100.0%; Score 57; DB 3; Length 57;
 Best Local Similarity 89.5%; Pred. No. 2.9e-07;
 Matches 51; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGUCCACCUCCUCCGCGGNNNNNNNUGGCAUGCCUUCGGCAUGGCUAAGGGACCC 57
 Db 1 GGGUCCACCUCCUCCGCGGCGCGACCGUCCUUCGGCAUGGCUAAGGGACCC 57
 RESULT 2
 AA257636
 ID AA257636 standard; RNA; 57 BP.
 AC AA257636;
 XX
 DT 05-APR-2000 (first entry)
 DE Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
 XX
 DE Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
 KW inherited disease; deltaRzP1.1; ss.
 KW
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT misc_binding 1..6
 FT /tag= a
 FT /note= "Forms double stranded region with bases 52-57"
 FT stem_loop 7..19
 FT /tag= b
 FT misc_binding 20..25
 FT /tag= c
 FT /bound_moiety= "SP1.1 substrate (AA257641) bases 5-11"
 FT stem_loop 30..45
 FT /tag= d
 FT misc_binding 52..57
 FT /tag= e
 FT /note= "Forms a double stranded region with bases 6-1"
 XX
 PN WO9955856-A2.
 XX
 XX 04-NOV-1999.
 XX
 XX 29-APR-1999; 99WO-CA000391.
 XX
 XX 29-APR-1998; 98CA-02230203.
 PR
 XX (UYSH) UNIV SHERBROOKE.
 PA
 XX

PI Perreault J, Ananvoranich S, Lafontaine D;
 XX WPI; 2000-096791/08.
 XX New construction of nucleic acid enzyme useful for biotechnological,
 PT diagnostic and therapeutic applications.
 XX Example 1; Fig 1A; 52pp; English.
 XX This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
 CC cleaves substrate SP1.1 (see AA257641). The invention relates to a
 CC nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
 CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
 CC substrate of the enzyme has the sequence 5'-H*GNNHN-3'. The binding
 CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
 CC cleavage site of the substrate (cleavage site is represented by *). At
 CC least one nucleotide is present 5' to the cleavage site of the substrate
 CC sequence. The enzyme of the invention is used to cleave a substrate
 CC nucleotide sequence at a specific cleavage site by mixing the substrate
 CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
 CC for example an inherited disease. The enzymes also have other
 CC therapeutic, biotechnological and diagnostic applications
 XX
 SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
 Query Match 83.2%; Score 47.4; DB 3; Length 57;
 Best Local Similarity 78.9%; Pred. No. 0.00032;
 Matches 45; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GGGUCCACCUCCUCCGCGGNNNNNNNUGGCAUGCCUUCGGCAUGGCUAAGGGACCC 57
 Db 1 GGGUCCACCUCCUCCGCGGCGCGACCGUCCUUCGGCAUGGCUAAGGGACCC 57
 RESULT 3
 AA257637
 ID AA257637 standard; RNA; 57 BP.
 AC AA257637;
 XX
 DT 05-APR-2000 (first entry)
 DE Trans-acting antigenomic delta ribozyme, deltaRzP1.2 nucleotide sequence.
 XX
 DE Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
 KW inherited disease; deltaRzP1.2; ss.
 KW
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT misc_binding 1..6
 FT /tag= a
 FT /note= "Forms double stranded region with bases 52-57"
 FT stem_loop 7..19
 FT /tag= b
 FT misc_binding 20..25
 FT /tag= c
 FT /bound_moiety= "SP1.2 substrate bases (AA257634) 6-11"
 FT stem_loop 30..45
 FT /tag= d
 FT misc_binding 52..57
 FT /tag= e
 FT /note= "Forms a double stranded region with bases 6-1"
 XX
 PN WO9955856-A2.
 XX
 XX 04-NOV-1999.
 XX
 XX 29-APR-1999; 99WO-CA000391.
 XX
 XX 29-APR-1998; 98CA-02230203.
 PR
 XX (UYSH) UNIV SHERBROOKE.
 PA

CC recombinant virus can efficiently express the antigen of hepatitis B
 CC virus with the safety and immunogenicity of attenuated encephalitis B
 CC virus vaccines. The current sequence represents a PCR primer used in an
 CC example from the invention.

XX
 SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 51.6%; Score 29.4; DB 13; Length 48;
 Best Local Similarity 58.1%; Pred. No. 1.5e+02;
 Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCGCAUGC 34
 :||||:||||:||||:||||:||||: |
 Db 17 TCCACCTCTCGCGGTCCGACCTGGGCATCC 47

RESULT 8
 AAQ86204
 ID AAQ86204 standard; DNA; 52 BP.

XX AAQ86204;

XX AC

XX 25-MAR-2003 (revised)

DT 23-NOV-1995 (first entry)

XX Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.

XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.

XX Synthetic.

OS

PN WO9507994-A2.

XX

PD 23-MAR-1995.

XX 15-SEP-1994; 94WO-US010469.

XX 15-SEP-1993; 93US-00122791.

PR 18-FEB-1994; 94US-00198450.

XX (VIAG-) VIAGENE INC.

PA Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;

XX WPI; 1995-131362/17.

DR

XX New alpha virus vectors for gene therapy - of viral infection, cancer,

PT auto-immune disease, etc., and as vaccines.

XX Example 7; Page 114; 260pp; English.

XX The sequences given in AAQ86200-15 are primers which were used in the

CC production of alphavirus vectors expressing multiple heterologous genes.

CC These vectors are eukaryotic layered vector initiation systems (ELVIS)

CC derived from Sindbis. ELVIS's comprise a 5' sequence capable of

CC initiating transcription of an alphavirus, a nucleotide sequence encoding

CC alphavirus non-structural proteins, a viral junction region which has

CC been inactivated such that viral transcription of the subgenomic fragment

CC is prevented, and an alphavirus RNA polymerase recognition sequence.

CC Inactivation of the viral junction region prevents transcription of the

CC subgenomic fragment making vectors such as this suitable for a wide

CC variety of applications, eg. gene therapy for the treatment of cystic

CC fibrosis. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 51.6%; Score 29.4; DB 2; Length 52;

Best Local Similarity 58.1%; Pred. No. 1.5e+02;

Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

XX

XX

XX

XX

XX

XX

XX

XX

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCGCAUGC 34
 :||||:||||:||||:||||:||||: |
 Db 17 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 9

AAAT31151

ID AAAT31151 standard; DNA; 52 BP.

XX AC

XX AAAT31151;

XX 12-SEP-1996 (first entry)

DT HDV reverse primer HDV17-68.

XX

XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine;

KW polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;

KW ribozyme; ss.

XX Synthetic.

OS

PN WO9617072-A2.

XX

XX 06-JUN-1996.

PD

XX 30-NOV-1995; 95WO-US015490.

XX

XX 30-NOV-1994; 94US-00348472.

PR 18-JAN-1995; 95US-00376184.

PR 15-MAR-1995; 95US-00405827.

XX

XX (CHIR) CHIRON VIAGENE INC.

PA

XX Dubensky TW, Polo JM, Ibanez CE, Chang SM, Jolly DJ, Driver DA;

XX Belli BA;

XX WPI; 1996-277785/28.

DR

XX New recombinant alpha-virus vectors - used to develop prods and methods

PT for use in gene therapy and in the prodn. of vaccines.

XX Example 7; Page 120; 256pp; English.

XX

XX Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)

CC nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)

CC for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV

CC (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment

CC contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping

CC synthesis is used in a second round of PCR using primers HDV49-XC and

CC SIN276-SPE. The resulting construct contains the expression cassette

CC elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction

CC region/Sindbis structural protein genes/Sindbis 3'-end untranslated

CC region, designated pDS'268. This was inserted into pCDNA3. Packaging cell

CC line cassettes were constructed that allow inducible expression of

CC structural proteins via alphavirus vectors

XX

SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 51.6%; Score 29.4; DB 2; Length 52;

Best Local Similarity 58.1%; Pred. No. 1.5e+02;

Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

XX

XX

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XX

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XX

```
DT 12-SEP-1996 (first entry)
XX HDV ribozyme primer HDV17-68.
XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;
KW polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;
KW hepatitis delta virus; ss.
XX Synthetic.
XX WO9617072-A2.
XX 06-JUN-1996.
XX 30-NOV-1995; 95WO-US015490.
XX 30-NOV-1994; 94US-00348472.
XX 18-JAN-1995; 95US-00376184.
XX 15-MAR-1995; 95US-00405827.
XX (CHIR ) CHIRON VIAGENE INC.
XX Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;
PI Belli BA;
XX WPI; 1996-277785/28.
XX New recombinant alpha-virus vectors - used to develop prods and methods
PT for use in gene therapy and in the prodn. of vaccines.
XX Example 3; Page 85; 256pp; English.
XX Primer SHDV1F (AAT30816) contains a buffer sequence allowing enzyme
CC digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme
CC sequence. It was used with nested primer HDV17-68 (AAT30817) and reverse
CC primer SHDV84R (AAT30818) to generate an HDV ribozyme. This antigenomic
CC ribozyme can be placed between the polyA tract at the 3' end of a Sindbis
CC virus-based eukaryotic layered vector initiation system, ELVIS, and the
CC transcription terminal signals to produce alphavirus expression vectors
CC useful in methods of gene therapy and for vaccine prodn
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
SQ Query Match 51.6%; Score 29.4; DB 2; Length 52;
Best Local Similarity 58.1%; Pred. No. 1.6e+02;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCCGCGGNNNNNNNUGGCGAUGC 34
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCCTCGCGGTCCGACCTGGGCATCC 31

RESULT 11
AAV42394
ID AAV42394 standard; DNA; 52 BP.
XX
XX AAV42394;
AC AAV42394;
XX
XX 02-OCT-1998 (first entry)
DT
XX Nested PCR primer HDV17-68 of the invention.
DE
XX DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; PCR primer; ss.
XX Synthetic.
XX US5789245-A.
XX 04-AUG-1998.
XX
XX 30-OCT-1996; 96US-00741881.
XX
XX DNA alpha:virus structural protein expression cassettes - for producing
```

```
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX (CHIR ) CHIRON CORP.
XX
XX Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX WPI; 1998-446089/38.
XX
XX DNA alpha:virus structural protein expression cassettes - for producing
PT recombinant alpha:virus particles.
XX Example 3; Col 69; 140pp; English.
XX
XX PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC invention. The specification describes a DNA alphavirus structural
CC protein expression cassette which comprises an inducible promoter and an
CC alphavirus structural protein gene, where the promoter directs the
CC expression of the alphavirus structural protein gene upon induction of
CC the promoter within a cell, and where prior to induction within the cell,
CC the expression cassette does not express sufficient quantities of
CC structural proteins to be cytotoxic to a BHK cell containing the
CC expression cassette. The products may be used to inhibit pathogens and
CC stimulate an immune response
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
SQ Query Match 51.6%; Score 29.4; DB 2; Length 52;
Best Local Similarity 58.1%; Pred. No. 1.6e+02;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCCGCGGNNNNNNNUGGCGAUGC 34
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCCTCGCGGTCCGACCTGGGCATCC 31

RESULT 12
AAV42426
ID AAV42426 standard; DNA; 52 BP.
XX
XX AAV42426;
AC AAV42426;
XX
XX 02-OCT-1998 (first entry)
DT
XX Forward PCR primer HDV17-68.
DE
XX DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; PCR primer; ss.
XX Synthetic.
XX US5789245-A.
XX 04-AUG-1998.
XX
XX 30-OCT-1996; 96US-00741881.
XX
XX 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX (CHIR ) CHIRON CORP.
XX
XX Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX WPI; 1998-446089/38.
XX
XX DNA alpha:virus structural protein expression cassettes - for producing
```

PT recombinant alpha:virus particles.
 XX Example 7; Col 103; 140pp; English.
 CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and an
 CC alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the cell,
 CC the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 51.6%; Score 29.4; DB 2; Length 52;
 Best Local Similarity 58.1%; Pred. No. 1.6e+02;
 Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUCCGCGGNNNNNNNNUGGCGAUGC 34
 :|||||:|||||:|||||:|||||:|||||:|
 Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCC 31
 RESULT 13
 AAV60154
 ID AAV60154 standard; DNA; 52 BP.
 XX
 AC AAV60154;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 XX Nested PCR primer HDV17-68.
 DE
 XX Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 XX
 XX Synthetic.
 OS Hepatitis D virus.
 XX
 XX US5814482-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 30-OCT-1996; 96US-00739158.
 XX
 XX 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 XX (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 PI WPI; 1998-541753/46.
 XX
 XX Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 XX Example 3; Col 71-72; 144pp; English.
 PS
 XX PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
 CC ribozyme sequence. The product is used in the course of the invention.

CC The specification describes an eukaryotic layered vector initiation
 CC system, based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
 CC The RNA comprises a vector construct which autonomously amplifies in the
 CC cell and expresses a heterologous nucleic acid sequence which encodes an
 CC antigen or modified form that stimulates an immune response within an
 CC animal. The system is useful for stimulating an immune response to an
 CC antigen by introducing the vector into target cells, preferably by
 CC infection in vivo, especially where the immune response is a cell
 CC mediated, HLA class I-restricted or an HLA class II-restricted immune
 CC response. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 51.6%; Score 29.4; DB 2; Length 52;
 Best Local Similarity 58.1%; Pred. No. 1.6e+02;
 Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUCCGCGGNNNNNNNNUGGCGAUGC 34
 :|||||:|||||:|||||:|||||:|||||:|
 Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCC 31
 RESULT 14
 AAV60185
 ID AAV60185 standard; DNA; 52 BP.
 XX
 AC AAV60185;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 XX Reverse PCR primer HDV17-68.
 DE
 XX Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 XX
 XX Synthetic.
 OS
 XX US5814482-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 30-OCT-1996; 96US-00739158.
 XX
 XX 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 XX (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 PI WPI; 1998-541753/46.
 XX
 XX Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 XX Example 5; Col 108; 144pp; English.
 PS
 XX PCR primers AAV60184-85 are used in the course of the invention. The
 CC specification describes an eukaryotic layered vector initiation system,
 CC based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.

CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 51.6%; Score 29.4; DB 2; Length 52;
Best Local Similarity 58.1%; Pred. No. 1.6e+02;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCGAUGC 34
:|||||:|||||:|||||:|||||:|||||:|
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

RESULT 15
AAV70746
ID AAV70746 standard; DNA; 52 BP.
XX
AC AAV70746;
XX
DT 20-MAR-2003 (revised)
DT 02-FEB-1999 (first entry)
XX
DE Reverse PCR primer HDV17-68 used to amplify Hepatitis delta virus.
XX
KW Alphavirus vector construct; gene therapy; PCR primer; ss.
XX
OS Synthetic.
OS Hepatitis D virus.
XX
PN US5843723-A.
XX
PD 01-DEC-1998.
XX
PF 30-OCT-1996; 96US-00739167.
XX
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 20-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chang SMW, Jolly DJ, Dubensky TW, Belli BA, Ibanez CE, Driver DA;
PI Polo JM;
XX
DR WPI; 1999-044581/04.
XX
PT Alphavirus vectors constructs containing a 5' promoter of viral cDNA by
PT in vitro transcription - used in gene therapy.
XX
PS Example 7; Col 103; 140pp; English.
XX
CC PCR primers AAV70745-46 are used to amplify part of the hepatitis delta
CC virus (HDV) genome. The amplified product is used in the production of
CC the alphavirus vector constructs of the invention. These constructs
CC comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA
CC from the viral cDNA by in vitro transcription, followed by a 5' sequence
CC which initiates transcription of alphavirus RNA, followed by a nucleotide
CC sequence encoding alphavirus nonstructural proteins, a viral junction
CC region which has been inactivated such that viral transcription of a
CC subgenomic fragment is prevented, an internal ribosome entry site or a
CC sequence which promotes ribosome read through between adjacent reading
CC frames, and an alphavirus RNA polymerase recognition sequence. The
CC recombinant alphavirus vectors can be used for gene therapy. (Updated on
CC 20-MAR-2003 to correct PR field.)

XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 51.6%; Score 29.4; DB 2; Length 52;
Best Local Similarity 58.1%; Pred. No. 1.6e+02;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCGAUGC 34
:|||||:|||||:|||||:|||||:|||||:|
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCC 31

Search completed: March 15, 2005, 16:13:01
Job time : 317.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:52:23 ; Search time 130.614 Seconds
(without alignments)
910.856 Million cell updates/sec

Title: US-09-699-667E-66

Perfect score: 20

Sequence: 1 bkegcauggcuaggagacc 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 5307542

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
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20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	80.0	25	19	US-10-719-900-844389
2	14.8	74.0	25	19	US-10-719-900-387639
3	14.4	72.0	25	19	US-10-719-900-844390
4	13.8	69.0	25	19	US-10-719-900-453629
5	13.8	69.0	48	17	US-10-346-880-41
6	13.8	69.0	48	17	US-10-150-407-41
7	13.8	69.0	56	17	US-10-346-880-79
8	13.8	69.0	56	17	US-10-150-407-79
9	13.6	68.0	25	15	US-10-098-263B-12150
10	13.6	68.0	25	19	US-10-719-900-157223
11	13.6	68.0	25	19	US-10-719-900-637105

c	12	13.6	68.0	31	19	US-10-855-975-18	Sequence 18, Appl
c	13	13.6	68.0	35	10	US-09-047-966-80	Sequence 80, Appl
c	14	13.6	68.0	43	10	US-09-047-966-81	Sequence 81, Appl
	15	13.6	68.0	47	10	US-09-993-346-282	Sequence 282, App
	16	13.4	67.0	17	15	US-10-060-895A-394	Sequence 394, App
	17	13.4	67.0	17	15	US-10-060-895A-395	Sequence 395, App
	18	13.4	67.0	17	15	US-10-060-895A-396	Sequence 396, App
	19	13.4	67.0	20	16	US-10-331-907-306	Sequence 306, App
	20	13.4	67.0	25	15	US-10-060-895A-1163	Sequence 1163, Ap
	21	13.4	67.0	25	15	US-10-060-895A-1164	Sequence 1164, Ap
	22	13.4	67.0	25	15	US-10-060-895A-1165	Sequence 1165, Ap
	23	13.4	67.0	25	15	US-10-060-895A-1166	Sequence 1166, Ap
	24	13.4	67.0	25	15	US-10-060-895A-1167	Sequence 1167, Ap
	25	13.4	67.0	25	15	US-10-060-895A-1168	Sequence 1168, Ap
	26	13.4	67.0	25	15	US-10-060-895A-1169	Sequence 1169, Ap
	27	13.4	67.0	25	15	US-10-060-895A-1170	Sequence 1170, Ap
	28	13.4	67.0	25	15	US-10-060-895A-1171	Sequence 1171, Ap
	29	13.4	67.0	25	15	US-10-060-895A-1172	Sequence 1172, Ap
	30	13.4	67.0	25	15	US-10-060-895A-1173	Sequence 1173, Ap
c	31	13.4	67.0	25	19	US-10-719-900-142538	Sequence 142538,
c	32	13.4	67.0	25	19	US-10-719-900-499116	Sequence 499116,
c	33	13.4	67.0	25	19	US-10-719-900-659058	Sequence 659058,
c	34	13.4	67.0	40	16	US-10-331-907-307	Sequence 307, App
c	35	13.2	66.0	25	19	US-10-719-900-387640	Sequence 387640,
c	36	13.2	66.0	41	17	US-10-035-833A-1043	Sequence 1043, Ap
c	37	13.2	66.0	41	17	US-10-035-833A-3396	Sequence 3396, Ap
c	38	13	65.0	17	15	US-10-060-895A-397	Sequence 397, App
c	39	13	65.0	17	15	US-10-060-895A-398	Sequence 398, App
c	40	13	65.0	24	10	US-09-940-185-1956	Sequence 1956, Ap
c	41	13	65.0	25	15	US-10-060-895A-1174	Sequence 1174, Ap
c	42	13	65.0	25	15	US-10-060-895A-1175	Sequence 1175, Ap
c	43	13	65.0	25	19	US-10-719-900-340671	Sequence 340671,
c	44	13	65.0	25	19	US-10-719-900-835115	Sequence 835115,
c	45	13	65.0	25	19	US-10-719-900-961898	Sequence 961898,

ALIGNMENTS

RESULT 1
US-10-719-900-844389
; Sequence 844389, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-844389

Query Match 80.0%; Score 16; DB 19; Length 25;
Best Local Similarity 87.5%; Pred. No. 26+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 19

Db 5 GCATGGCTAAGGACC 20

||||:|||||

||||:|||||

RESULT 2

US-10-719-900-387639

; Sequence 387639, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 387639
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-387639

Query Match 74.0%; Score 14.8; DB 19; Length 25;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 18
Db 2 TGGCGATGGCTTAGAGAC 19

RESULT 3
US-10-719-900-844390
Sequence 844390, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 844390
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-844390

Query Match 72.0%; Score 14.4; DB 19; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 19
Db 5 GCATGGCTTAGGACC 20

RESULT 4
US-10-719-900-453629
Sequence 453629, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 453629
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-453629

Query Match 69.0%; Score 13.8; DB 19; Length 25;
Best Local Similarity 76.5%; Pred. No. 2.8e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 20
Db 7 GCCTGGCTAAGGGAACC 23

RESULT 5
US-10-346-880-41/c
Sequence 41, Application US/10346880
Publication No. US20030232035A1
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W
APPLICANT: Polo, John M
APPLICANT: Ibanez, Carlos E
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J
APPLICANT: Driver, David A
APPLICANT: Belli, Barbara A
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
CURRENT APPLICATION NUMBER: US/10/346,880
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: 09/503,138
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/191,747
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 08/739,199
PRIOR FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: 08/404,796
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: 08/376,184
PRIOR FILING DATE: 1995-01-18
PRIOR APPLICATION NUMBER: 08/348,472
PRIOR FILING DATE: 1994-11-30
PRIOR APPLICATION NUMBER: 08/198,450
PRIOR APPLICATION NUMBER: 08/122,791
PRIOR FILING DATE: 1993-09-15
NUMBER OF SEQ ID NOS: 128
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 41
LENGTH: 48
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Artificial sequence: reverse primer SHDV84R
US-10-346-880-41

Query Match 69.0%; Score 13.8; DB 17; Length 48;
Best Local Similarity 64.7%; Pred. No. 2.7e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17
Db 29 CTCGGATGGCTTAGGGA 13

RESULT 6
US-10-150-407-41/c
Sequence 41, Application US/10150407
Publication No. US20040029278A1
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP


```
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-150-407-41
Query Match 69.0%; Score 13.8; DB 17; Length 48;
Best Local Similarity 64.7%; Pred. No. 2.7e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17
Db 29 CTCGGATGGCTAAGGGA 13

RESULT 7
US-10-346-880-79/c
; Sequence 79, Application US/10346880
; Publication No. US2003023035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
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; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: forward primer HDV49-XC
US-10-346-880-79
Query Match 69.0%; Score 13.8; DB 17; Length 56;
Best Local Similarity 64.7%; Pred. No. 2.7e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17
Db 37 CTCGGATGGCTAAGGGA 21

RESULT 8
US-10-150-407-79/c
; Sequence 79, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-150-407-79
Query Match 69.0%; Score 13.8; DB 17; Length 56;
Best Local Similarity 64.7%; Pred. No. 2.7e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17
Db 37 CTCGGATGGCTAAGGGA 21
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 637105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-637105
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Query Match      68.0%; Score 13.6; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.6e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY 1 BKSGCAUGGCUAAGGACCC 20
   ::|||::|||::|||
Db 20 CTGGCATGGCTTAGGAGCCC 1
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RESULT 12

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US-10-855-975-18/c
; Sequence 18, Application US/10855975
; Publication No. US20050037487A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kawaoka, Yoshihiro
; APPLICANT: Hamm, Stefan
; APPLICANT: Ebihara, Hideki
; TITLE OF INVENTION: WARF - Wisconsin Alumni Research Foundation
; TITLE OF INVENTION: Recombinant Influenza Vectors with A PolII Promoter and Ribozymes
; FILE REFERENCE: 800.037US1
; CURRENT APPLICATION NUMBER: US/10/855,975
; CURRENT FILING DATE: 2004-05-27
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic primer
US-10-855-975-18
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Query Match      68.0%; Score 13.6; DB 19; Length 31;
Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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QY 2 KSGCAUGGCUAAGGGA 17
   ::|||::|||::|||
Db 31 TCGGATGGCTAAGGGA 16
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RESULT 13

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US-09-047-966-80
; Sequence 80, Application US/09047966
; Publication No. US20030138773A1
; GENERAL INFORMATION:
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; APPLICANT: J. Gordon Foulkes, et al.
; TITLE OF INVENTION: Methods of Transcriptionally
; TITLE OF INVENTION: Modulating Gene Expression.
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: John P. White, Esq.
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 100036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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RESULT 9

```
US-10-098-263B-12150
; Sequence 12150, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
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; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12150
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-12150
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Query Match      68.0%; Score 13.6; DB 15; Length 25;
Best Local Similarity 65.0%; Pred. No. 3.6e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

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QY 1 BKSGCAUGGCUAAGGACCC 20
   ::|||::|||::|||
Db 1 TTGGAACGGTTAAGGAGCCC 20
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RESULT 10

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US-10-719-900-157223/c
; Sequence 157223, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 157223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-157223
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Query Match      68.0%; Score 13.6; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.6e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY 1 BKSGCAUGGCUAAGGACCC 20
   ::|||::|||::|||
Db 21 CTGGCTTGGTTAAGGAGCTC 2
```

RESULT 11

```
US-10-719-900-637105/c
; Sequence 637105, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
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QY 1 BKSGCAUGGCUAAGGACCC 20

Db :::| |||:||||| ||
28 GGGGAAGGGCTAAGGAGCC 47

Search completed: March 15, 2005, 21:09:26
Job time : 131.614 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:59:13 ; Search time 244.395 Seconds
(without alignments)
900.574 Million cell updates/sec

Title: US-09-699-667E-65

Perfect score: 37

Sequence: 1 ggguccacucccgcggunnnnnnggcaugcaby 37

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	81.1	52	17	US-10-346-880-40
2	30	81.1	52	17	US-10-346-880-40
3	30	81.1	52	17	US-10-346-880-40
4	30	81.1	52	17	US-10-150-407-40
5	30	81.1	90	9	US-09-733-042-12
6	30	81.1	90	9	US-09-733-042-12
7	30	81.1	90	10	US-09-190-246-2
8	30	81.1	91	15	US-10-237-302-7
9	30	81.1	99	15	US-10-237-302-8
10	30	81.1	5451	18	US-10-485-281-6
11	30	81.1	8100	10	US-09-190-246-4
					Sequence 40, Appl
					Sequence 80, Appl
					Sequence 40, Appl
					Sequence 80, Appl
					Sequence 12, Appl
					Sequence 13, Appl
					Sequence 2, Appl
					Sequence 7, Appl
					Sequence 8, Appl
					Sequence 6, Appl
					Sequence 4, Appl

12	30	81.1	15538	10	US-09-190-246-1	Sequence 1, Appl
13	29	78.4	56	10	US-09-507-362-39	Sequence 39, Appl
14	29	78.4	56	17	US-10-391-441-39	Sequence 39, Appl
15	28.4	76.8	2583	18	US-10-441-926-35	Sequence 35, Appl
16	28	75.7	842	16	US-10-252-157-493	Sequence 493, Appl
17	28	75.7	1137	18	US-10-770-668-37	Sequence 37, Appl
18	28	75.7	4846	18	US-10-648-593-33	Sequence 33, Appl
19	28	75.7	4711	15	US-10-084-817-183	Sequence 183, Appl
20	28	75.7	4732	16	US-10-133-013-17	Sequence 17, Appl
21	27.4	74.1	1172	18	US-10-425-115-21586	Sequence 21586, A
22	27.4	74.1	1613	18	US-10-739-930-2810	Sequence 2810, Ap
23	27.4	74.1	2583	18	US-10-441-926-34	Sequence 34, Appl
24	27.4	74.1	2583	18	US-10-441-926-36	Sequence 36, Appl
25	27.4	74.1	2583	18	US-10-441-926-40	Sequence 40, Appl
26	27.4	74.1	2583	18	US-10-441-926-41	Sequence 41, Appl
27	27.4	74.1	2583	18	US-10-441-926-42	Sequence 42, Appl
28	27	73.0	49	9	US-09-812-186-5	Sequence 5, Appl
29	27	73.0	49	10	US-09-961-077-1234	Sequence 1234, Ap
30	27	73.0	49	13	US-10-103-480-9	Sequence 9, Appl
31	27	73.0	49	15	US-10-156-433-38	Sequence 38, Appl
32	27	73.0	49	16	US-10-112-814-38	Sequence 38, Appl
33	27	73.0	110	19	US-10-855-975-25	Sequence 25, Appl
34	27	73.0	604	18	US-10-767-701-22134	Sequence 22134, A
35	27	73.0	1831	17	US-10-310-154-359	Sequence 359, App
36	26.8	72.4	313	9	US-09-867-701-4302	Sequence 4302, Ap
37	26.8	72.4	1005	15	US-10-156-761-716	Sequence 716, App
38	26.8	72.4	1498	18	US-10-425-115-1871	Sequence 1871, Ap
39	26.8	72.4	9025608	15	US-10-156-761-1	Sequence 1, Appl
40	26.6	71.9	311	10	US-09-764-891-9829	Sequence 9829, Ap
41	26.6	71.9	455	13	US-10-027-632-257756	Sequence 257756, Ap
42	26.6	71.9	455	13	US-10-027-632-257757	Sequence 257757, Ap
43	26.6	71.9	455	17	US-10-027-632-257756	Sequence 257756, Ap
44	26.6	71.9	455	17	US-10-027-632-257757	Sequence 257757, Ap
45	26.6	71.9	4741	10	US-09-764-891-9828	Sequence 9828, Ap

ALIGNMENTS

RESULT 1

US-10-346-880-40
; Sequence 40, Application US/10346880
; Publication No. US2003023035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146 213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 40
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match      81.1%; Score 30; DB 17; Length 52;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGUNNNNNNGGCAUGCS 35
Db 1 TCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 2
US-10-346-880-80
; Sequence 80, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

Query Match      81.1%; Score 30; DB 17; Length 52;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGUNNNNNNGGCAUGCS 35
Db 1 TCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 3
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
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; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-150-407-40

Query Match      81.1%; Score 30; DB 17; Length 52;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGUNNNNNNGGCAUGCS 35
Db 1 TCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 4
US-10-150-407-80
; Sequence 80, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/150,407
;   FILING DATE: 17-May-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/350,522
;   FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
;   NAME: McWaters, David D.
;   REGISTRATION NUMBER: 33,963
;   REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 52 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-150-407-80

      Query Match      81.1%; Score 30; DB 17; Length 52;
      Best Local Similarity 56.2%; Pred. No. 9.8;
      Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACUCCUCCGCGGNNNNNNNGGCGAUGCS 35
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Db      1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 5
US-09-733-042-12
; Sequence 12, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
;   APPLICANT: Hennecke, Frank
;   TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
;   FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-FOR
US-09-733-042-12

      Query Match      81.1%; Score 30; DB 9; Length 90;
      Best Local Similarity 56.2%; Pred. No. 9.7;
      Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACUCCUCCGCGGNNNNNNNGGCGAUGCS 35
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Db      22 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 53

RESULT 6
US-09-733-042-13/C
; Sequence 13, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
;   APPLICANT: Hennecke, Frank
;   TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
;   FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
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; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-REV
US-09-733-042-13

      Query Match      81.1%; Score 30; DB 9; Length 90;
      Best Local Similarity 56.2%; Pred. No. 9.7;
      Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACUCCUCCGCGGNNNNNNNGGCGAUGCS 35
      :|||||:|||||:|||||:|||||:|||||:
Db      73 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 42

RESULT 7
US-09-190-246-2
; Sequence 2, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
;   APPLICANT: Parrington, Mark
;   APPLICANT: Li, Xiaomao
;   APPLICANT: Klein, Michel
;   TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
;   FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-2

      Query Match      81.1%; Score 30; DB 10; Length 90;
      Best Local Similarity 56.2%; Pred. No. 9.7;
      Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACUCCUCCGCGGNNNNNNNGGCGAUGCS 35
      :|||||:|||||:|||||:|||||:|||||:
Db      22 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 53

RESULT 8
US-10-237-302-7
; Sequence 7, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
;   APPLICANT: Alphavax, Inc.
;   APPLICANT: Jonathan F. Smith
;   APPLICANT: Kurt I. Kamrud
;   APPLICANT: Jonathan O. Rayner
;   APPLICANT: Sergey A. Drysa
;   APPLICANT: Ian J. Caley
;   TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
;   FILE REFERENCE: 01113.000202
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
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; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match      81.1%; Score 30; DB 15; Length 91;
Best Local Similarity 56.2%; Pred. No. 9.7;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGCGGNNNNNNNGGCGAUGCS 35
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Db 18 TCACCTCTCGCGGTCCGACCTGGGCATCCG 49

RESULT 9
US-10-237-302-8/c
; Sequence 8, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 0113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-8

Query Match      81.1%; Score 30; DB 15; Length 99;
Best Local Similarity 56.2%; Pred. No. 9.7;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGCGGNNNNNNNGGCGAUGCS 35
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Db 78 TCACCTCTCGCGGTCCGACCTGGGCATCCG 47

RESULT 10
US-10-485-281-6
; Sequence 6, Application US/10485281
; Publication No. US20040265821A1
; GENERAL INFORMATION:
; APPLICANT: Sandig, Volker
; APPLICANT: Jordan, Ingo
; TITLE OF INVENTION: RNA Amplification System Using Plant Components in
; FILE REFERENCE: 040026US/JH
; CURRENT APPLICATION NUMBER: US/10/485,281
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: PCT/DE02/02863
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5451
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Vector p100-79
US-10-485-281-6

; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match      81.1%; Score 30; DB 15; Length 91;
Best Local Similarity 56.2%; Pred. No. 9.7;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGCGGNNNNNNNGGCGAUGCS 35
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Db 18 TCACCTCTCGCGGTCCGACCTGGGCATCCG 49

RESULT 9
US-10-237-302-8/c
; Sequence 8, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 0113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-8

Query Match      81.1%; Score 30; DB 15; Length 99;
Best Local Similarity 56.2%; Pred. No. 9.7;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGCGGNNNNNNNGGCGAUGCS 35
   :|||||:|||||:|||||:|||||:|||||:|
Db 78 TCACCTCTCGCGGTCCGACCTGGGCATCCG 47

RESULT 10
US-10-485-281-6
; Sequence 6, Application US/10485281
; Publication No. US20040265821A1
; GENERAL INFORMATION:
; APPLICANT: Sandig, Volker
; APPLICANT: Jordan, Ingo
; TITLE OF INVENTION: RNA Amplification System Using Plant Components in
; FILE REFERENCE: 040026US/JH
; CURRENT APPLICATION NUMBER: US/10/485,281
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: PCT/DE02/02863
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5451
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Vector p100-79
US-10-485-281-6

; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match      81.1%; Score 30; DB 18; Length 5451;
Best Local Similarity 56.2%; Pred. No. 8.6;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGCGGNNNNNNNGGCGAUGCS 35
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Db 5002 TCACCTCTCGCGGTCCGACCTGGGCATCCG 5033

RESULT 11
US-09-190-246-4
; Sequence 4, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Semliki Forest virus
; OTHER INFORMATION: Semliki Forest virus
US-09-190-246-4

Query Match      81.1%; Score 30; DB 10; Length 8100;
Best Local Similarity 56.2%; Pred. No. 8.5;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

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Db 8032 TCACCTCTCGCGGTCCGACCTGGGCATCCG 8063

RESULT 12
US-09-190-246-1
; Sequence 1, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15538
; TYPE: DNA
; ORGANISM: Semliki Forest virus
; OTHER INFORMATION: Semliki Forest virus
US-09-190-246-1

Query Match      81.1%; Score 30; DB 10; Length 15538;
Best Local Similarity 56.2%; Pred. No. 8.4;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGCGGNNNNNNNGGCGAUGCS 35
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RESULT 13
US-09-507-362-39
; Sequence 39, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
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; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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; US-09-507-362-39
;
; Query Match 78.4%; Score 29; DB 10; Length 56;
; Best Local Similarity 58.6%; Pred. No. 23;
; Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
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; QY 4 UCCACUCCUCCGGGUNNNNNNGGCAU 32
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; Db 27 TCCACCTCTCGCGTCCGACCTGGCAT 55
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; RESULT 14
; US-10-391-441-39
; Sequence 39, Application US/10391441
; Publication No. US20030232058A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,441
; FILING DATE: 17-Mar-2003
; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match 78.4%; Score 29; DB 17; Length 5
Best Local Similarity 58.6%; Pred. No. 23;
Matches 17; Conservative 12; Mismatches 0; Indels

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DB 27 TCCACCTCTCGCGTCGCGACCTGGGCAT 55

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; Sequence 35, Application US/10441926
; Publication No. US20040115621A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-011001
; CURRENT APPLICATION NUMBER: US/10/441,926
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 2583
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated oligonucleotide
US-10-441-926-35

Query Match 76.8%; Score 28.4; DB 18; Length
Best Local Similarity 50.0%; Pred. No. 35;
Matches 18; Conservative 14; Mismatches 4; Indels

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GenCore version 5.1.6
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Perfect score: 37
Sequence: 1 ggguccaccuccgcggunnnnnnggcaugsby 37

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 5307542

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	81.1	52	17	US-10-346-880-40 Sequence 40, Appl
2	30	81.1	52	17	US-10-346-880-80 Sequence 80, Appl
3	30	81.1	52	17	US-10-150-407-40 Sequence 40, Appl
4	30	81.1	52	17	US-10-150-407-80 Sequence 80, Appl
5	29	78.4	56	17	US-09-507-362-39 Sequence 39, Appl
6	29	78.4	56	17	US-10-391-441-39 Sequence 39, Appl
7	27	73.0	49	9	US-09-812-186-5 Sequence 5, Appl
8	27	73.0	49	10	US-09-961-077-1234 Sequence 1234, Ap
9	27	73.0	49	13	US-10-103-480-9 Sequence 9, Appl
10	27	73.0	49	15	US-10-156-433-38 Sequence 38, Appl
11	27	73.0	49	16	US-10-112-814-38 Sequence 38, Appl

C	12	22.4	60.5	32	18	US-10-363-552-29	Sequence 29, Appl
C	13	22.4	60.5	39	10	US-09-991-262-7	Sequence 7, Appl
C	14	22.4	60.5	60	10	US-09-908-975-18325	Sequence 18325, A
C	15	22	59.5	33	10	US-09-864-636A-381	Sequence 381, App
C	16	22	59.5	33	10	US-09-864-636A-382	Sequence 382, App
C	17	22	59.5	33	11	US-09-864-426A-381	Sequence 381, App
C	18	22	59.5	33	11	US-09-864-426A-382	Sequence 382, App
C	19	22	59.5	33	16	US-10-084-839-381	Sequence 381, App
C	20	22	59.5	33	16	US-10-084-839-382	Sequence 382, App
C	21	21.8	58.9	25	19	US-10-719-900-867275	Sequence 867275,
C	22	21.8	58.9	31	10	US-09-999-2208-28	Sequence 28, Appl
C	23	21.8	58.9	31	10	US-09-999-2208-85	Sequence 85, Appl
C	24	21.8	58.9	31	10	US-09-999-2208-97	Sequence 97, Appl
C	25	21.6	58.4	51	18	US-10-813-638-704	Sequence 704, Appl
C	26	21.6	58.4	29	9	US-09-848-464-8	Sequence 8, Appl
C	27	21.6	58.4	46	14	US-10-136-841-19	Sequence 19, Appl
C	28	21.6	58.4	46	17	US-10-272-531A-19	Sequence 19, Appl
C	29	21.6	58.4	46	17	US-10-272-483A-19	Sequence 19, Appl
C	30	21.6	58.4	51	18	US-10-628-109-118	Sequence 118, App
C	31	21.6	58.4	55	18	US-10-628-109-106	Sequence 106, App
C	32	21.6	58.4	55	18	US-10-628-109-107	Sequence 107, App
C	33	21.6	58.4	55	18	US-10-628-109-108	Sequence 108, App
C	34	21.6	58.4	60	10	US-09-908-975-6071	Sequence 6071, Ap
C	35	21.6	58.4	60	10	US-09-908-975-20076	Sequence 20076, A
C	36	21.4	57.8	39	8	US-08-978-806-3	Sequence 3, Appl
C	37	21.4	57.8	39	9	US-09-972-834-3	Sequence 3, Appl
C	38	21.4	57.8	39	17	US-10-670-184-161	Sequence 161, App
C	39	21.4	57.8	41	17	US-10-277-216-256	Sequence 256, App
C	40	21.4	57.8	41	17	US-10-126-022-256	Sequence 256, App
C	41	21.4	57.8	51	17	US-10-393-815-80	Sequence 80, Appl
C	42	21.2	57.3	36	14	US-10-244-715-22	Sequence 22, Appl
C	43	21.2	57.3	41	16	US-10-224-683-45	Sequence 45, Appl
C	44	21.2	57.3	41	17	US-10-035-833A-3312	Sequence 2312, Ap
C	45	21.2	57.3	41	17	US-10-035-833A-3718	Sequence 3718, Ap

ALIGNMENTS

RESULT 1

US-10-346-880-40
; Sequence 40, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 40
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match      81.1%; Score 30; DB 17; Length 52;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGCGGNNNNNGGCGCAUGCS 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 2
US-10-346-880-80
; Sequence 80, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

Query Match      81.1%; Score 30; DB 17; Length 52;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGCGGNNNNNGGCGCAUGCS 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 3
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; SEQ ID NO 40
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match      81.1%; Score 30; DB 17; Length 52;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGCGGNNNNNGGCGCAUGCS 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 4
US-10-150-407-80
; Sequence 80, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 622-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-150-407-80

Query Match      81.1%; Score 30; DB 17; Length 52;
Best Local Similarity 56.2%; Pred. No. 9.8;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNNNGGCGAUCG 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGCGATCCG 32

RESULT 5
US-09-507-362-39
; Sequence 39, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
; Frollov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
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; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 622-6031
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match      78.4%; Score 29; DB 17; Length 56;
Best Local Similarity 58.6%; Pred. No. 23;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNNNGGCGCAU 32
   :|||||:|||||:|||||:|||||:
Db 27 TCCACCTCTCGCGGTCCGACCTGGCGAT 55

RESULT 6
US-10-391-441-39
; Sequence 39, Application US/10391441
; Publication No. US20030232058A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
; Frollov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,441
; FILING DATE: 17-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 622-6031
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match      78.4%; Score 29; DB 17; Length 56;
Best Local Similarity 58.6%; Pred. No. 23;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNNNGGCGCAU 32
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Db 27 TCCACCTCTCGCGGTCCGACCTGGCGAT 55
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RESULT 7
US-09-812-186-5
; Sequence 5, Application US/09812186
; Patent No. US20020052037A1
; GENERAL INFORMATION:
; APPLICANT: BRIGELMAN, LEONID
; TITLE OF INVENTION: NUCLEIC ACID CATALYSTS COMPRISING L-NUCLEOTIDE ANALOGS
; FILE REFERENCE: MBH00-922-A
; CURRENT APPLICATION NUMBER: US/09/812,186
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/042,464
; PRIOR FILING DATE: 1997-03-31
; PRIOR APPLICATION NUMBER: 09/048,825
; PRIOR FILING DATE: 1998-03-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hepatitis
; NAME/KEY: misc feature
; LOCATION: (18)-(24)
; OTHER INFORMATION: all n's can represent any one of a, c, g, or u
US-09-812-186-5

Query Match          73.0%; Score 27; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNNGGC 30
Db 2 UCCACCUCUCGCGGUNNNNNNGGC 28

RESULT 8
US-09-961-077-1234
; Sequence 1234, Application US/09961077
; Publication No. US20030014775A1
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; Edington, Brent E.
; McSwiggen, James A.
; Merlo, Patricia Ann Owens
; Guo, Lining
; Skokut, Thomas A.
; Young, Scott A.
; Folkerts, Otto
; Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; MODULATION OF GENE EXPRESSION
; IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,077
; FILING DATE: 21-Sep-2001
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1234:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The letter "N" stands for any base.
SEQUENCE DESCRIPTION: SEQ ID NO: 1234:
US-09-961-077-1234

Query Match          73.0%; Score 27; DB 10; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNNGGC 30
Db 2 UCCACCUCUCGCGGUNNNNNNGGC 28

RESULT 9
US-10-103-480-9
; Sequence 9, Application US/10103480
; Publication No. US20020192685A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Thompson, Jim
; TITLE OF INVENTION: Method For Target Site Selection and Discovery
; FILE REFERENCE: MBH00.1286-A 900/001
; CURRENT APPLICATION NUMBER: US/10/103,480
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 09/112,086
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: US 09/108,087
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,718
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (18)-(24)
; OTHER INFORMATION: n stands for any a, c, g, or u
US-10-103-480-9

Query Match          73.0%; Score 27; DB 13; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNNGGC 30
Db 2 UCCACCUCUCGCGGUNNNNNNGGC 28
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RESULT 11
US-10-112-814-38
; Sequence 38, Application US/10112814
; Publication No. US20030170644A1
; GENERAL INFORMATION:
; APPLICANT: Alex. Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Bellon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-943-D; 400.005
; CURRENT APPLICATION NUMBER: US/10/112,814
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 38

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RESULT 13
US-09-991-262-7
; Sequence 7, Application US/09991262
; Publication No. US20030041349A1
; GENERAL INFORMATION:
; APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
; TITLE OF INVENTION: Insect Viruses and Their Uses in
; Protecting Plants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/991,262
APPLICATION NUMBER: US/09/991,262
FILING DATE: 20-NO. US20030041349A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/234,238
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: US 08/485,355
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-3/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-991-262-7

Query Match 60.5%; Score 22.4; DB 10; Length 39;
Best Local Similarity 58.3%; Pred. No. 7.3e+03;
Matches 14; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCUCCUGCGGUNNNNNNGGCA 31
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Db 16 CCTCTCGCGCGCGGATGGCA 39

RESULT 14

US-09-908-975-18325/c
Sequence 18325, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 18325
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens

US-09-908-975-18325

Query Match 60.5%; Score 22.4; DB 10; Length 60;
Best Local Similarity 50.0%; Pred. No. 7.2e+03;
Matches 16; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGUCCACCUCCUGCGGUNNNNNNGGCAUG 33
||:|||||:|||||:|||||:|||||
Db 53 GGTCCACATCCACACAGATGGCCTTGAGCATG 22

RESULT 15

US-09-864-636A-381/c
Sequence 381, Application US/09864636A
Publication No. US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allwai, Hatim
APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT APPLICATION NUMBER: US/09/864,636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 381
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-381

Query Match 59.5%; Score 22; DB 10; Length 33;
Best Local Similarity 53.3%; Pred. No. 1e+04;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGUCCACCUCCUGCGGUNNNNNNGGCA 31
||:|||||:|||||:|||||:|||||
Db 31 GGTCCACCTCCAGAGGAGGTCGGTGGCA 2

Search completed: March 15, 2005, 21:09:25
Job time : 242.636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:59:13 ; Search time 132.105 Seconds
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900.574 Million cell updates/sec

Title: US-09-699-667E-64
Perfect score: 20
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Scoring table: IDENTITY NUCDX
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Searched: 5537552 seqs, 2974263231 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	85.0	20190	10	US-09-996-015-3
2	17	85.0	20190	17	US-10-287-190-167
3	17	85.0	20190	17	US-10-307-817-153
C 4	17	85.0	135005	18	US-10-723-860-2320
C 5	16.8	84.0	572	13	US-10-027-632-231346
C 6	16.8	84.0	572	17	US-10-027-632-231346
7	16.8	84.0	1786	10	US-09-993-966-1
8	16.8	84.0	1859	10	US-09-993-966-5
9	16.8	84.0	2922	10	US-09-374-048A-93
10	16.8	84.0	2922	17	US-10-616-263-93
C 11	16.8	84.0	202802	17	US-10-085-117-286

12	16.4	82.0	1380	9	US-09-738-626-2903	Sequence 2303, Ap
13	16.4	82.0	1543	19	US-10-494-541-9	Sequence 9, Appli
C 14	16.4	82.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
15	16	80.0	25	19	US-10-719-900-844389	Sequence 844389,
C 16	15.8	79.0	201	18	US-10-719-993-53406	Sequence 53406, A
C 17	15.8	79.0	442	17	US-10-424-599-53225	Sequence 53225, A
C 18	15.8	79.0	708	13	US-10-027-632-98682	Sequence 98682, A
C 19	15.8	79.0	708	17	US-10-027-632-98682	Sequence 98682, A
C 20	15.8	79.0	2320	10	US-09-946-374-281	Sequence 281, App
C 21	15.8	79.0	2320	14	US-10-006-856A-281	Sequence 281, App
C 22	15.8	79.0	2320	14	US-10-006-818A-281	Sequence 281, App
C 23	15.8	79.0	2320	14	US-10-006-485A-281	Sequence 281, App
C 24	15.8	79.0	2320	14	US-10-013-907A-281	Sequence 281, App
C 25	15.8	79.0	2320	14	US-10-015-499A-281	Sequence 281, App
C 26	15.8	79.0	2320	14	US-10-015-393A-281	Sequence 281, App
C 27	15.8	79.0	2320	14	US-10-015-869A-281	Sequence 281, App
C 28	15.8	79.0	2320	14	US-10-012-121A-281	Sequence 281, App
C 29	15.8	79.0	2320	14	US-10-006-116A-281	Sequence 281, App
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C 33	15.8	79.0	2320	14	US-10-007-194A-281	Sequence 281, App
C 34	15.8	79.0	2320	14	US-10-013-430A-281	Sequence 281, App
C 35	15.8	79.0	2320	14	US-10-011-671A-281	Sequence 281, App
C 36	15.8	79.0	2320	14	US-10-012-758A-281	Sequence 281, App
C 37	15.8	79.0	2320	14	US-10-015-386A-281	Sequence 281, App
C 38	15.8	79.0	2320	15	US-10-011-692A-281	Sequence 281, App
C 39	15.8	79.0	2320	15	US-10-006-768A-281	Sequence 281, App
C 40	15.8	79.0	2320	15	US-10-017-610A-281	Sequence 281, App
C 41	15.8	79.0	2320	15	US-10-006-063A-281	Sequence 281, App
C 42	15.8	79.0	2320	15	US-10-020-063A-281	Sequence 281, App
C 43	15.8	79.0	2320	15	US-10-015-391A-281	Sequence 281, App
C 44	15.8	79.0	2320	15	US-10-017-407A-281	Sequence 281, App
C 45	15.8	79.0	2320	15	US-10-011-833A-281	Sequence 281, App

ALIGNMENTS

RESULT 1
US-09-996-015-3
; Sequence 3, Application US/09996015
; Publication No. US20030032166A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Pena, Carol A. E.
; APPLICANT: Li, Li
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Leite, Mario W.
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 15966-581 CIP
; CURRENT APPLICATION NUMBER: US/09/996, 015
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 09/641,741
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2206)
; OTHER INFORMATION: Wherein n is A, C, G, or T
; FEATURE:

NAME/KEY: misc_feature
LOCATION: (2207)
OTHER INFORMATION: Wherein n is A, C, G, or T
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2209)
OTHER INFORMATION: Wherein n is A, C, G, or T
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2211)
OTHER INFORMATION: Wherein n is A, C, G, or T
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2214)
OTHER INFORMATION: Wherein n is A, C, G, or T
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2215)
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (2221)
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NAME/KEY: misc_feature
LOCATION: (2222)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (2224)
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NAME/KEY: misc_feature
LOCATION: (2226)
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (2229)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (2230)
OTHER INFORMATION: Wherein n is A, C, G, or T

Query Match 85.0%; Score 17; DB 10; Length 20190;
Best Local Similarity 88.2%; Pred. No. 54;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGGA 17
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DB 20059 GCGCATGGCTAAGGGA 20075

RESULT 2
US-10-287-190-167
; Sequence 167, Application US/10287190
; Publication No. US20040038230A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-780B
CURRENT APPLICATION NUMBER: US/10/287,190
CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 09/996,015
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/338626
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/373806
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/338196
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/333912
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/381043
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/401593
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: 60/334300
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 194
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 167
LENGTH: 20190
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2202)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2206)..(2206)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2207)..(2207)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2209)..(2209)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2211)..(2211)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2214)..(2214)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2215)..(2215)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2218)..(2218)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2220)..(2220)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2221)..(2221)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2222)..(2222)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2224)..(2224)
OTHER INFORMATION: Wherein n may be a, c, g or t
FEATURE:

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;/ NAME/KEY: misc_feature
;/ LOCATION: (2226)..(2226)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (2227)..(2227)
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;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (2229)..(2229)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (2230)..(2230)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
US-10-287-190-167
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Query Match      85.0%; Score 17; DB 17; Length 20190;
Best Local Similarity 88.2%; Pred. No. 54;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GCGCGAUGGCUAAGGGA 17
      |||||:|||||
Db      20059 GCGCATGCTAAGGGA 20075
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RESULT 3

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US-10-307-817-153
; Sequence 153, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 153
; LENGTH: 20190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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;/ NAME/KEY: CDS
;/ LOCATION: (1)..(2202)
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (2206)..(2206)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
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;/ NAME/KEY: misc_feature
;/ LOCATION: (2207)..(2207)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (2209)..(2209)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (2211)..(2211)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
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;/ NAME/KEY: misc_feature
;/ LOCATION: (2214)..(2214)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
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;/ NAME/KEY: misc_feature
;/ LOCATION: (2215)..(2215)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (2218)..(2218)
;/ OTHER INFORMATION: Wherein n may be a, c, g or t
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;/ FEATURE:
;/ NAME/KEY: misc_feature
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;/ FEATURE:
;/ NAME/KEY: misc_feature
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;/ OTHER INFORMATION: Wherein n may be a, c, g or t
US-10-307-817-153
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Query Match      85.0%; Score 17; DB 17; Length 20190;
Best Local Similarity 88.2%; Pred. No. 54;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GCGCGAUGGCUAAGGGA 17
      |||||:|||||
Db      20059 GCGCATGCTAAGGGA 20075
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RESULT 4

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US-10-723-860-2320/c
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320
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Query Match      85.0%; Score 17; DB 18; Length 135005;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GCGCGAUGGCUAAGGGA 17
      |||||:|||||
Db      108776 GCGCATGCTAAGGGA 108760
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RESULT 5
US-10-027-632-231346/c
; Sequence 231346, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231346
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231346

Query Match      84.0%; Score 16.8; DB 13; Length 572;
Best Local Similarity 85.0%; Pred. No. 87;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCGCGAUGGCUAAGGACCC 20
DB      120  GGCACAGGGCTAAGGACCC 101

RESULT 6
US-10-027-632-231346/c
; Sequence 231346, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231346
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231346

Query Match      84.0%; Score 16.8; DB 13; Length 572;
Best Local Similarity 85.0%; Pred. No. 87;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCGCGAUGGCUAAGGACCC 20
DB      120  GGCACAGGGCTAAGGACCC 101
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231346

Query Match      84.0%; Score 16.8; DB 17; Length 572;
Best Local Similarity 85.0%; Pred. No. 87;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCGCGAUGGCUAAGGACCC 20
DB      120  GGCACAGGGCTAAGGACCC 101

RESULT 7
US-09-993-966-1
; Sequence 1, Application US/09993966
; Publication No. US20030186232A1
; GENERAL INFORMATION:
; APPLICANT: ROHAN, MICHAEL
; TITLE OF INVENTION: HUMAN AND NON-HUMAN PRIMATE HOMOLOGUES OF NKD PROTEIN,
; NUCLEIC ACID SEQUENCES ENCODING, AND USES THEREOF
; FILE REFERENCE: 014024/0280733
; CURRENT APPLICATION NUMBER: US/09/993,966
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/252,884
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/291,109
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/325,571
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-993-966-1

Query Match      84.0%; Score 16.8; DB 10; Length 1786;
Best Local Similarity 80.0%; Pred. No. 80;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCGCGAUGGCUAAGGACCC 20
DB      117  GCGCGATGGCTTAGGACGC 136

RESULT 8
US-09-993-966-5
; Sequence 5, Application US/09993966
; Publication No. US20030186232A1
; GENERAL INFORMATION:
; APPLICANT: ROHAN, MICHAEL
; TITLE OF INVENTION: HUMAN AND NON-HUMAN PRIMATE HOMOLOGUES OF NKD PROTEIN,
; NUCLEIC ACID SEQUENCES ENCODING, AND USES THEREOF
; FILE REFERENCE: 014024/0280733
; CURRENT APPLICATION NUMBER: US/09/993,966
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/252,884
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/291,109
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/325,571
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-993-966-5

Query Match      84.0%; Score 16.8; DB 10; Length 1859;
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Best Local Similarity 80.0%; Pred. No. 80;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGGACCC 20
Db 182 GGCGCATGGCTTAGGACGC 201

RESULT 9
US-09-374-046A-93
; Sequence 93, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2922
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-374-046A-93

Query Match 84.0%; Score 16.8; DB 10; Length 2922;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGGACCC 20
Db 2466 GGCGCATGGCTTAGACCC 2485

RESULT 10
US-10-616-263-93
; Sequence 93, Application US/10616263
; Publication No. US20040038276A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000103.5
; CURRENT APPLICATION NUMBER: US/10/616,263
; CURRENT FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0

Best Local Similarity 80.0%; Pred. No. 80;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGGACCC 20
Db 2466 GGCGCATGGCTTAGACCC 2485

RESULT 11
US-10-085-117-286/c
; Sequence 286, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 52945200021
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 202802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-286

Query Match 84.0%; Score 16.8; DB 17; Length 202802;
Best Local Similarity 80.0%; Pred. No. 58;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGGACCC 20
Db 16256 GGACATGGCTTAGGGACCC 16237

RESULT 12
US-09-738-626-2903
; Sequence 2903, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIRO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2903
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; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2903

Query Match      82.0%; Score 16.4; DB 9; Length 1380;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGGAC 18
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Db 161 GGCTCATGGCTAAGGGAC 178

RESULT 13
US-10-494-541-9
; Sequence 9, Application US/10494541
; Publication No. US2005009152A1
; GENERAL INFORMATION:
; APPLICANT: Zelder, Oskar
; APPLICANT: Pompejus, Markus
; APPLICANT: Schroder, Hartwig
; APPLICANT: Kroger, Burkhard
; APPLICANT: Klopprogge, Corinna
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: Gene coding for proteins for genetic stability,
; FILE REFERENCE: BGI-166US
; CURRENT APPLICATION NUMBER: US/10/494,541
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: PCT/EP02/12138
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: DE 10154180
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 9
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1513)
; OTHER INFORMATION: RXA00314
US-10-494-541-9

Query Match      82.0%; Score 16.4; DB 19; Length 1543;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGGAC 18
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Db 294 GGCTCATGGCTAAGGGAC 311

RESULT 14
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match      82.0%; Score 16.4; DB 9; Length 3309400;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGGAC 18
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Db 2809618 GGCTCATGGCTAAGGGAC 2809601

RESULT 15
US-10-719-900-844389
; Sequence 844389, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-844389

Query Match      80.0%; Score 16; DB 19; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGGACC 19
    ||| |||:|||||
Db 5 GCATGGCTAAGGGACC 20

Search completed: March 15, 2005, 15:52:07
Job time : 139.105 secs
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:52:23 ; Search time 130.614 Seconds
(without alignments)
910.856 Million cell updates/sec

Title: US-09-699-667E-64

Perfect score: 20

Sequence: 1 ggcgcagggcuaggagacc 20

Scoring table: IDENTITY NUCDX

Gapop 10_0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 5307542

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	25	19	US-10-719-900-844389
2	14.4	72.0	25	19	US-10-719-900-844390
3	14.2	71.0	37	9	US-09-982-246-54
4	14.2	71.0	37	18	US-10-681-822-54
5	13.8	69.0	17	10	US-09-740-332-1546
6	13.8	69.0	17	10	US-09-817-879-1546
7	13.8	69.0	17	18	US-10-669-841-4139
8	13.8	69.0	24	10	US-09-940-185-1956
9	13.8	69.0	25	19	US-10-719-900-387639
10	13.8	69.0	25	19	US-10-719-900-453629
11	13.8	69.0	60	10	US-09-908-975-11788

C	12	13.6	68.0	25	19	US-10-719-900-204642	Sequence 204642,
	13	13.6	68.0	25	19	US-10-719-900-788103	Sequence 788103,
	14	13.6	68.0	35	10	US-09-047-966-80	Sequence 80, Appl
C	15	13.6	68.0	35	14	US-10-146-835-33	Sequence 33, Appl
	16	13.6	68.0	43	10	US-09-047-966-81	Sequence 81, Appl
C	17	13.6	68.0	47	10	US-09-993-346-282	Sequence 282, App
	18	13.4	67.0	17	15	US-10-060-895A-394	Sequence 394, App
	19	13.4	67.0	17	15	US-10-060-895A-395	Sequence 395, App
	20	13.4	67.0	17	15	US-10-060-895A-396	Sequence 396, App
	21	13.4	67.0	20	16	US-10-331-907-306	Sequence 306, App
	22	13.4	67.0	25	15	US-10-060-895A-1163	Sequence 1163, Ap
	23	13.4	67.0	25	15	US-10-060-895A-1164	Sequence 1164, Ap
	24	13.4	67.0	25	15	US-10-060-895A-1165	Sequence 1165, Ap
	25	13.4	67.0	25	15	US-10-060-895A-1166	Sequence 1166, Ap
	26	13.4	67.0	25	15	US-10-060-895A-1167	Sequence 1167, Ap
	27	13.4	67.0	25	15	US-10-060-895A-1168	Sequence 1168, Ap
	28	13.4	67.0	25	15	US-10-060-895A-1169	Sequence 1169, Ap
	29	13.4	67.0	25	15	US-10-060-895A-1170	Sequence 1170, Ap
	30	13.4	67.0	25	15	US-10-060-895A-1171	Sequence 1171, Ap
	31	13.4	67.0	25	15	US-10-060-895A-1172	Sequence 1172, Ap
	32	13.4	67.0	25	15	US-10-060-895A-1173	Sequence 1173, Ap
C	33	13.4	67.0	25	19	US-10-719-900-499116	Sequence 499116,
	34	13.4	67.0	25	19	US-10-719-900-659058	Sequence 659058,
C	35	13.4	67.0	31	19	US-10-855-975-18	Sequence 18, Appl
	36	13.4	67.0	40	16	US-10-331-907-307	Sequence 307, App
	37	13.4	67.0	48	17	US-10-346-880-41	Sequence 41, Appl
	38	13.4	67.0	48	17	US-10-150-407-41	Sequence 41, Appl
	39	13.4	67.0	56	17	US-10-346-880-79	Sequence 79, Appl
C	40	13.4	67.0	56	17	US-10-150-407-79	Sequence 79, Appl
	41	13.2	66.0	25	10	US-09-864-636A-1857	Sequence 1857, Ap
	42	13.2	66.0	25	11	US-09-864-426A-1857	Sequence 1857, Ap
C	43	13.2	66.0	25	15	US-10-098-263B-12150	Sequence 12150, A
	44	13.2	66.0	25	16	US-10-084-839-1857	Sequence 1857, Ap
C	45	13.2	66.0	25	19	US-10-719-900-62677	Sequence 62677, A

ALIGNMENTS

RESULT 1
US-10-719-900-844389
; Sequence 844389, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-844389

Query Match 80.0%; Score 16; DB 19; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 19

Db 5 GCATGGCTAAGGACC 20

RESULT 2

US-10-719-900-844390
; Sequence 844390, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

/ APPLICANT: Xue Mei Zhou
 / TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 / FILE REFERENCE: 3528.1
 / CURRENT APPLICATION NUMBER: US/10/719,900
 / CURRENT FILING DATE: 2003-11-20
 / PRIOR APPLICATION NUMBER: 60/427,808
 / PRIOR FILING DATE: 2002 11 20
 / NUMBER OF SEQ ID NOS: 982914
 / SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 / SEQ ID NO 844390
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Mus musculus
 / US-10-719-900-844390

Query Match 72.0%; Score 14.4; DB 19; Length 25;
 Best Local Similarity 81.2%; Pred. No. 1.8e+03;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACC 19
 |||:||||: |||||
 DB 5 GCATGGCTTAGGACC 20

RESULT 3

/ US-09-882-246-54
 / Sequence 54, Application US/09882246
 / Patent No. US20020106652A1
 / GENERAL INFORMATION:
 / APPLICANT: GOLD, LARRY
 / WILLIS, MICHAEL
 / KOCH, TAD
 / RINGQUIST, STEVEN
 / JENSEN, KIRK
 / ATKINSON, BRENT
 / TITLE OF INVENTION: SYSTEMATIC EVOLUTION
 / OF
 / LIGANDS BY EXPONENTIAL
 / ENRICHMENT: PHOTSELECTION
 / NUMBER OF SEQUENCES: 64
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Swanson & Bratschun, L.L.C.
 / STREET: 8400 E. Prentice Avenue, Suite 200
 / CITY: Englewood
 / STATE: Colorado
 / COUNTRY: USA
 / ZIP: 80111
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
 / storage
 / COMPUTER: IBM
 / OPERATING SYSTEM: MS-DOS
 / SOFTWARE: WordPerfect 8.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/882,246
 / FILING DATE: 14-Jun-2001
 / CLASSIFICATION: <Unknown>
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 09/093,293
 / FILING DATE: <Unknown>
 / APPLICATION NUMBER: PCT/US94/10542
 / FILING DATE: 18 September 1994
 / APPLICATION NUMBER: 08/123,935
 / FILING DATE: 17 September 1993
 / APPLICATION NUMBER: 08/143,564
 / FILING DATE: 25 October 1993
 / APPLICATION NUMBER: 07/714,131
 / FILING DATE: 10 JUNE 1991
 / APPLICATION NUMBER: 07/536,428
 / FILING DATE: 11 JUNE 1990
 / APPLICATION NUMBER: 07/931,473
 / FILING DATE: 17 AUGUST 1992
 / ATTORNEY/AGENT INFORMATION:

/ NAME: Barry J. Swanson
 / REGISTRATION NUMBER: 33,215
 / REFERENCE/DOCKET NUMBER: NEX10/US-CON
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (303) 793-3333
 / TELEFAX: (303) 793-3433
 / INFORMATION FOR SEQ ID NO: 54:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 37 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / SEQUENCE DESCRIPTION: SEQ ID NO: 54:
 / US-09-882-246-54

Query Match 71.0%; Score 14.2; DB 9; Length 37;
 Best Local Similarity 84.2%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACC 19
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 DB 12 GCGCACGGAUAGGACC 30

RESULT 4

/ US-10-681-822-54
 / Sequence 54, Application US/10681822
 / Publication No. US20040132067A1
 / GENERAL INFORMATION:
 / APPLICANT: GOLD, LARRY
 / WILLIS, MICHAEL
 / KOCH, TAD
 / RINGQUIST, STEVEN
 / JENSEN, KIRK
 / ATKINSON, BRENT
 / TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF
 / LIGANDS BY EXPONENTIAL
 / ENRICHMENT: PHOTSELECTION
 / OF NUCLEIC ACID LIGANDS AND
 / NUMBER OF SEQUENCES: 64
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Swanson & Bratschun, L.L.C.
 / STREET: 8400 E. Prentice Avenue, Suite 200
 / CITY: Englewood
 / STATE: Colorado
 / COUNTRY: USA
 / ZIP: 80111
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
 / storage
 / COMPUTER: IBM
 / OPERATING SYSTEM: MS-DOS
 / SOFTWARE: WordPerfect 8.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/10/681,822
 / FILING DATE: 10-Aug-2003
 / CLASSIFICATION: <Unknown>
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: NUMBER:US/09/093,293
 / FILING DATE: 08-June 1998
 / APPLICATION NUMBER: 08/612,895
 / FILING DATE: 03 August 1996
 / APPLICATION NUMBER: PCT/US94/10542
 / FILING DATE: 18 September 1994
 / APPLICATION NUMBER: 08/123,935
 / FILING DATE: 17 September 1993
 / APPLICATION NUMBER: 08/143,564
 / FILING DATE: 25 October 1993
 / APPLICATION NUMBER: 07/714,131
 / FILING DATE: 10 JUNE 1991
 / APPLICATION NUMBER: 07/536,428
 / FILING DATE: 11 JUNE 1990
 / APPLICATION NUMBER: 07/931,473


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; FILING DATE: 17 AUGUST 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX10/US-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-681-822-54

Query Match          71.0%; Score 14.2; DB 18; Length 37;
Best Local Similarity 84.2%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGCGAUGGCUAAGGACC 19
Db 12 GGGCGACGGAUAGGACC 30

RESULT 5
US-09-740-332-1546
; Sequence 1546, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis B Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1546
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1546

Query Match          69.0%; Score 13.8; DB 10; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGCGAUGGCUAAGGGA 17
Db 1 GGCUCGUGGCUAAGGGA 17

RESULT 6
US-09-817-879-1546
; Sequence 1546, Application US/09817879
; Publication No. US2003017311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1546
; LENGTH: 17
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; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1546

Query Match          69.0%; Score 13.8; DB 10; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGCGAUGGCUAAGGGA 17
Db 1 GGCUCGUGGCUAAGGGA 17

RESULT 7
US-10-669-841-4139
; Sequence 4139, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4139
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-4139

Query Match          69.0%; Score 13.8; DB 18; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGGA 17
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Db 1 GGCUUGGCUAAGGGA 17
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RESULT 8

US-09-940-185-1956

; Sequence 1956, Application US/09940185

; Publication No. US20030096239A1

; GENERAL INFORMATION:

; APPLICANT: Gunderson, Kevin

; APPLICANT: Chee, Mark

; TITLE OF INVENTION: Probes and Decoder Oligonucleotides

; FILE REFERENCE: A-69605-1

; CURRENT APPLICATION NUMBER: US/09/940,185

; CURRENT FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: US 60/227,948

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/228,854

; PRIOR FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 4768

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1956

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Computer Generated Probe Sequence.

US-09-940-185-1956

Query Match 69.0%; Score 13.8; DB 10; Length 24;

Best Local Similarity 82.4%; Pred. No. 3.7e+03;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCGAUGGCUAAGGAC 18
|||||:|||||
Db 1 GGCGACGCTAGGAC 17
|||||:|||||

RESULT 9

US-10-719-900-387639

; Sequence 387639, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 387639

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-387639

Query Match 69.0%; Score 13.8; DB 19; Length 25;

Best Local Similarity 76.5%; Pred. No. 3.7e+03;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGAUGGCUAAGGAC 18
|||||:|||||
Db 3 GGCGATGCTAGAGAC 19
|||||:|||||

RESULT 10

US-10-719-900-453629

; Sequence 453629, Application US/10719900

; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 453629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-453629

Query Match 69.0%; Score 13.8; DB 19; Length 25;

Best Local Similarity 76.5%; Pred. No. 3.7e+03;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACCC 20
|||:|||||
Db 7 GCCTGGCTAAGGGAACC 23
|||:|||||

RESULT 11

US-09-908-975-11788

; Sequence 11788, Application US/09908975

; Publication No. US20030165843A1

; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli

; APPLICANT: MINTZ, Liat

; APPLICANT: FAIGLER, Simchon

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING

; FILE REFERENCE: 36688-0005

; CURRENT APPLICATION NUMBER: US/09/908,975

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/287,724

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/221,607

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 32337

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 11788

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-908-975-11788

Query Match 69.0%; Score 13.8; DB 10; Length 60;

Best Local Similarity 76.5%; Pred. No. 3.5e+03;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGAUGGCUAAGGGA 17
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Db 23 GGCGCATGGCTTGGGGA 39
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RESULT 12

US-10-719-900-204642/c

; Sequence 204642, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

Search completed: March 15, 2005, 21:09:24
Job time : 132.614 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:59:13 ; Search time 244.395 Seconds
(without alignments)
900.574 Million cell updates/sec

Title: US-09-699-667E-63

Perfect score: 37
Sequence: 1 ggguccacucccgcggunnnmnnuggcaugccg 37

Scoring table: IDENTITY NUCDX
Gapop 10_0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.4	82.2	52	17	US-10-346-880-40
2	30.4	82.2	52	17	US-10-346-880-80
3	30.4	82.2	52	17	US-10-150-407-40
4	30.4	82.2	52	17	US-10-150-407-80
5	30.4	82.2	90	9	US-09-733-042-12
6	30.4	82.2	90	9	US-09-733-042-13
7	30.4	82.2	90	10	US-09-190-246-2
8	30.4	82.2	91	15	US-10-237-302-7
9	30.4	82.2	99	15	US-10-237-302-8
10	30.4	82.2	5451	18	US-10-485-281-6
11	30.4	82.2	8100	10	US-09-190-246-4

12	30.4	82.2	15538	10	US-09-190-246-1	Sequence 1, Appli
13	29	78.4	56	10	US-09-507-362-39	Sequence 39, Appli
14	29	78.4	56	17	US-10-391-441-39	Sequence 39, Appli
15	27	73.0	110	19	US-10-855-975-25	Sequence 25, Appli
16	26.6	71.9	311	10	US-09-764-891-9829	Sequence 9829, Ap
17	26.6	71.9	313	9	US-09-867-701-4302	Sequence 4302, Ap
18	26.6	71.9	2583	18	US-10-441-926-35	Sequence 35, Appli
19	26.6	71.9	4741	10	US-09-764-891-9828	Sequence 9828, Ap
20	26	70.3	992	17	US-10-369-493-37024	Sequence 37024, A
21	26	70.3	1137	18	US-10-770-668-37	Sequence 37, Appli
22	26	70.3	2226	11	US-09-968-007A-111	Sequence 111, App
23	26	70.3	2226	11	US-09-968-007A-731	Sequence 731, App
24	25.8	69.7	509	17	US-10-424-593-107007	Sequence 107007,
25	25.8	69.7	171096	18	US-10-612-869-8	Sequence 8, Appli
26	25.6	69.2	842	16	US-10-252-157-493	Sequence 493, App
27	25.6	69.2	2583	18	US-10-441-926-34	Sequence 34, Appli
28	25.6	69.2	2583	18	US-10-441-926-36	Sequence 36, Appli
29	25.6	69.2	2583	18	US-10-441-926-40	Sequence 40, Appli
30	25.6	69.2	2583	18	US-10-441-926-41	Sequence 41, Appli
31	25.6	69.2	2583	18	US-10-441-926-42	Sequence 42, Appli
32	25.6	69.2	4197	15	US-10-156-761-7203	Sequence 7203, Ap
33	25.6	69.2	4646	18	US-10-648-593-33	Sequence 33, Appli
34	25.6	69.2	4711	15	US-10-084-817-183	Sequence 183, App
35	25.6	69.2	4732	16	US-10-133-013-17	Sequence 17, Appli
36	25.6	69.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
37	25.4	68.6	500	15	US-10-106-698-3622	Sequence 3622, Ap
38	25.4	68.6	942	13	US-10-027-632-162439	Sequence 162439,
39	25.4	68.6	942	17	US-10-027-632-162439	Sequence 162439,
40	25.4	68.6	976	17	US-10-369-493-39564	Sequence 39564, A
41	25.4	68.6	1108	17	US-10-369-493-39192	Sequence 39192, A
42	25.4	68.6	1168	9	US-09-764-853-410	Sequence 410, App
43	25.4	68.6	1168	14	US-10-091-438-118	Sequence 118, App
44	25.4	68.6	1299	17	US-10-389-647-54	Sequence 54, Appli
45	25.4	68.6	1356	10	US-09-991-053-31	Sequence 31, Appli

ALIGNMENTS

RESULT 1

US-10-346-880-40
; Sequence 40, Application US/10346880
; Publication No. US2003023035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146 213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 40
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match      82.2%; Score 30.4; DB 17; Length 52;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCAUGCG 35
   :||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 2
US-10-346-880-80
; Sequence 80, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

Query Match      82.2%; Score 30.4; DB 17; Length 52;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCAUGCG 35
   :||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 3
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

US-10-150-407-80
; Sequence 80, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: McMahsters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-150-407-80

      Query Match      82.2%; Score 30.4; DB 17; Length 52;
      Best Local Similarity 59.4%; Pred. No. 2.7;
      Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
      :||||:||||:||||:||||:||||:||||:
Db      1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 5
US-09-733-042-12
; Sequence 12, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-FOR
US-09-733-042-12

      Query Match      82.2%; Score 30.4; DB 9; Length 90;
      Best Local Similarity 59.4%; Pred. No. 2.7;
      Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
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Db      22 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 53

RESULT 6
US-09-733-042-13/c
; Sequence 13, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
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;
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-REV
US-09-733-042-13

      Query Match      82.2%; Score 30.4; DB 9; Length 90;
      Best Local Similarity 59.4%; Pred. No. 2.7;
      Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
      :||||:||||:||||:||||:||||:||||:
Db      73 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 42

RESULT 7
US-09-190-246-2
; Sequence 2, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-2

      Query Match      82.2%; Score 30.4; DB 10; Length 90;
      Best Local Similarity 59.4%; Pred. No. 2.7;
      Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
      :||||:||||:||||:||||:||||:||||:
Db      22 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 53

RESULT 8
US-10-237-302-7
; Sequence 7, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: Alphavax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Drysa
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.000202
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
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; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match      82.2%; Score 30.4; DB 15; Length 91;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCG 35
Db 18 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 49

RESULT 9
US-10-237-302-8/c
; Sequence 8, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Calley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; PRIOR FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-237-302-8

Query Match      82.2%; Score 30.4; DB 15; Length 99;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCG 35
Db 78 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 47

RESULT 10
US-10-485-281-6
; Sequence 6, Application US/10485281
; Publication No. US20040265821A1
; GENERAL INFORMATION:
; APPLICANT: Sandig, Volker
; APPLICANT: Jordan, Ingo
; TITLE OF INVENTION: RNA Amplification System Using Plant Components in
; FILE REFERENCE: 040026us/JH
; CURRENT APPLICATION NUMBER: US/10/485,281
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: PCT/DE02/02863
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5451
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Vector p100-79
US-10-485-281-6

; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match      82.2%; Score 30.4; DB 15; Length 91;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCG 35
Db 18 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 49

RESULT 9
US-10-237-302-8/c
; Sequence 8, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Calley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; PRIOR FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-237-302-8

Query Match      82.2%; Score 30.4; DB 15; Length 99;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCG 35
Db 78 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 47

RESULT 10
US-10-485-281-6
; Sequence 6, Application US/10485281
; Publication No. US20040265821A1
; GENERAL INFORMATION:
; APPLICANT: Sandig, Volker
; APPLICANT: Jordan, Ingo
; TITLE OF INVENTION: RNA Amplification System Using Plant Components in
; FILE REFERENCE: 040026us/JH
; CURRENT APPLICATION NUMBER: US/10/485,281
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: PCT/DE02/02863
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5451
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Vector p100-79
US-10-485-281-6

; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match      82.2%; Score 30.4; DB 18; Length 5451;
Best Local Similarity 59.4%; Pred. No. 2.8;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCG 35
Db 5002 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 5033

RESULT 11
US-09-190-246-4
; Sequence 4, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Semliki Forest virus
; OTHER INFORMATION:
US-09-190-246-4

Query Match      82.2%; Score 30.4; DB 10; Length 8100;
Best Local Similarity 59.4%; Pred. No. 2.8;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCG 35
Db 8032 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 8063

RESULT 12
US-09-190-246-1
; Sequence 1, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15538
; TYPE: DNA
; ORGANISM: Semliki Forest virus
; OTHER INFORMATION:
US-09-190-246-1

Query Match      82.2%; Score 30.4; DB 10; Length 15538;
Best Local Similarity 59.4%; Pred. No. 2.8;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCG 35
Db 12479 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 12510

RESULT 13
US-09-507-362-39
; Sequence 39, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
```



```
;
;      Polo, John M.
;      Belli, Barbara A.
;      Schlesinger, Sondra
;      Dryga, Sergey A.
;      Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-507-362-39
;
; Query Match 78.4%; Score 29; DB 10; Length 56;
; Best Local Similarity 58.6%; Pred. No. 9.4;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 UCCACCUCUCGCGGNNNNNNUGGCAU 32
; :|||:|||||:|||||:|||||:
; Db 27 TCCACCTCTCGCGTCCGACCTGGGCAT 55
;
; RESULT 14
; US-10-391-441-39
; Sequence 39, Application US/10391441
; Publication No. US20030232058A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,441
; FILING DATE: 17-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39
;
; Query Match 78.4%; Score 29; DB 17; Length 56;
; Best Local Similarity 58.6%; Pred. No. 9.4;
; Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 UCCACCUCUCGCGGNNNNNNUGGCAU 32
; :|||:|||||:|||||:|||||:
; Db 27 TCCACCTCTCGCGTCCGACCTGGGCAT 55
;
; RESULT 15
; US-10-855-975-25
; Sequence 25, Application US/10855975
; Publication No. US20050037487A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoka, Yoshihiro
; APPLICANT: Hamm, Stefan
; APPLICANT: Ebihara, Hideki
; APPLICANT: WARF - Wisconsin Alumni Research Foundation
; TITLE OF INVENTION: Recombinant Influenza Vectors with A PolII Promoter and Ribozymes
; TITLE OF INVENTION: Vaccines and Gene Therapy
; FILE REFERENCE: 800.037US1
; CURRENT APPLICATION NUMBER: US/10/855,975
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,797
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 110
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic HDV ribozyme sequence
; US-10-855-975-25
;
; Query Match 73.0%; Score 27; DB 19; Length 110;
; Best Local Similarity 77.8%; Pred. No. 55;
; Matches 21; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 UCCACCUCUCGCGGNNNNNNUGGCG 30
; :|||:|||||:|||||:|||||:
; Db 67 UCCACCUCUCGCGGUGCCGACCGUGGC 93
;
; Search completed: March 15, 2005, 15:52:00
; Job time : 250.395 secs
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	27.4	74.1	534	8	BZ302458	BZ302458 KD1848.p1
2	27.4	74.1	673	5	BUE3843	BUE3843 603587131
C 3	27.4	74.1	993	4	BG911802	BG911802 602810016
C 4	27.2	73.5	746	9	AG412786	AG412786 Mus muscu
C 5	26.8	72.4	533	4	B1937265	B1937265 N31040BE1
C 6	26.6	71.9	331	1	AA421395	AA421395 zu27F02.r
C 7	26.6	71.9	343	2	BE453046	BE453046 894067H12
C 8	26.6	71.9	490	1	AV623815	AV623815 AV623815
C 9	26.6	71.9	492	2	BE855168	BE855168 6-11E-zo
C 10	26.6	71.9	529	7	CO897592	CO897592 pe03f12.y
C 11	26.6	71.9	549	7	BF861288	BF861288 psZQ0061E
C 12	26.6	71.9	597	2	CF431987	CF431987 nab93h11.
C 13	26.6	71.9	617	4	B1874134	B1874134 963113F07
C 14	26.6	71.9	754	2	BF860462	BF860462 963016F09
C 15	26.4	71.4	396	5	BQ360043	BQ360043 PM1-HN007
C 16	26.4	71.4	505	4	B1999774	B1999774 103107BE0
C 17	26.4	71.4	700	8	CC337252	CC337252 OGTAH36TV
C 18	26.4	71.4	714	4	BG857676	BG857676 1024053C1
C 19	26.4	71.4	732	2	BF303855	BF303855 601886656
C 20	26.4	71.4	854	9	CG351145	CG351145 OG3AD51TH
C 21	26.4	71.4	883	9	CC710615	CC710615 OGLAM65TV
C 22	26.4	71.4	899	2	BF673679	BF673679 602136403
C 23	26.4	71.4	917	9	CG625292	CG625292 OGUKO53TH
C 24	26.4	71.4	935	9	CG372347	CG372347 OG3DH25TH

from zoospores grown in liquid medium. Zoospores were released into water and collected by centrifugation at 2,000g; zoospore-bearing sporangia were induced to develop on 5 to 7 d old mycelium colonies grown on V8 agar by repeated flooding with water. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT) linker-primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amplified once using E. coli host strain XL1 Blue MRP⁺. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host strain XL0UR. Sequenced using T3 primer: 5' ATT AAC CCT CAC TAA AGG GA 3'.

ORIGIN

Query Match 71.9%; Score 26.6; DB 2; Length 492;
 Best Local Similarity 54.5%; Pred. No. 1.9e+03;
 Matches 18; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GUCCACUCCUCCGGGNNNNNUGGCGGCG 35
 :|||:|||:|||:|||:|||:|||:|||:|||
 Db 144 GTCTCTCTCTCGGGTGTGATGTCGCGCGCG 112

RESULT 10
LOCUS

CO897592 529 bp mRNA linear EST 13-AUG-2004
 pe03f12.y1 Radopholus similis SL1 TOPO v1 Radopholus similis cDNA
 5' similar to SW:1434_CABEL Q20855 14-3-3-LIKE PROTEIN 2. [1] ;
 mRNA sequence.

ACCESSION

CO897592

VERSION

CO897592.1 GI:51237382

KEYWORDS

EST.

SOURCE

Radopholus similis

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 Tylenchoidea; Pratylenchidae; Radopholinae; Radopholus.
 1 (bases 1 to 529)
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
 Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
 Tsagarashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
 Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

TITLE

Unpublished (1999)

JOURNAL

Contact: Mitreva M

COMMENT

The Washington Univ. Nematode EST Project, 2004
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Library constructed by: Irina Ronko and Dr. Makedonka Mitreva
 Seq primer: SL1 primer
 High quality sequence stop: 458.

FEATURES

source

1..529
 /organism="Radopholus similis"
 /mol_type="mRNA"
 /db_xref="taxon:46012"
 /dev_stage="Mixed"
 /lab_host="GC10"

/clone_lib="Radopholus similis SL1 TOPO v1"
 /note="Vector: pCRII-TOPO (Invitrogen); Site 1: 5': EcoRI;
 Site 2: 3': EcoRI; The library was constructed by Irina
 Ronko and Dr. Makedonka Mitreva
 (mitreva@wustl.edu) at Washington University, St.
 Louis. Oligo(dT)-SL1 PCR based library. Radopholus
 similis cDNA PCR products of size >400 nucleotides

containing SL1 on the 5' end and oligo(dT) on the 3' end
 were non-directionally cloned into pCRII-TOPO(Invitrogen)
 following the Topo TA cloning protocol. Radopholus similis
 total RNA was provided by Dr. Godelieve Gheysen of Ghent
 University (lighe@engp.rug.ac.be)."

ORIGIN

Query Match 71.9%; Score 26.6; DB 7; Length 529;
 Best Local Similarity 51.5%; Pred. No. 1.9e+03;
 Matches 17; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGGGNNNNNUGGCGGCG 36
 :|||:|||:|||:|||:|||:|||:|||:|||
 Db 321 TCCACCTTCTCGGGTACTCTTGGCCATCTGC 289

RESULT 11

LOCUS

CF861288 549 bp mRNA linear EST 31-OCT-2003
 psZ00061e11r Agriculture Canada Phytophthora sojae EST project_s20
 Phytophthora sojae cDNA clone sZ0006E11 5, mRNA sequence.

ACCESSION

CF861288

VERSION

CF861288.1 GI:38115914

KEYWORDS

EST.

SOURCE

Phytophthora sojae

ORGANISM

Phytophthora sojae

Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 Phytophthora.

REFERENCE

1 (bases 1 to 549)

AUTHORS

Qutob, D., Hraber, P. T., Sobral, B. W. S. and Gijzen, M.

TITLE

Comparative analysis of expressed sequences in Phytophthora sojae

JOURNAL

Plant Physiol. 123 (1), 243-254 (2000)

MEDLINE

20267956

PUBMED

10806241

COMMENT

Contact: Tyler B
 Tyler lab
 VBI
 1880 Pratt Dr., Blacksburg, VA 24061, USA
 Tel: 540-231-7318
 Email: bmtylex@vt.edu
 PCR Primers
 FORWARD: BK reverse primer
 BACKWARD: BK reverse primer
 Plate: 006 row: E column: 11
 Seq primer: BK reverse primer
 High quality sequence stop: 549.

FEATURES

source

1..549
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 /mol_type="mRNA"
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 /clone_lib="Agriculture Canada Phytophthora sojae EST
 project_s20"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 71.9%; Score 26.6; DB 7; Length 549;
 Best Local Similarity 54.5%; Pred. No. 1.9e+03;
 Matches 18; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GUCCACUCCUCCGGGNNNNNUGGCGGCG 35
 :|||:|||:|||:|||:|||:|||:|||:|||
 Db 153 GTCTCTCTCTCGGGTGTGATGTCGCGCGCG 121

RESULT 12

LOCUS

BF431987 597 bp mRNA linear EST 30-MAR-2001
 nab83h11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone


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1. .396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HNN0079"
/notes="Organ: head normal; Vector: puc18; Site 1: SmaI;

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Result No.	Score		Query Match		Length	DB	ID	Description
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1	57	100.0	57	100.0	3	AA257636	AA257636	Trans-act
2	57	100.0	57	100.0	3	AA257637	AA257637	Trans-act
3	47.4	83.2	57	83.2	3	AA257638	AA257638	Trans-act
4	35.4	62.1	37	62.1	3	AA257639	AA257639	Nucleotid
5	30.4	53.3	48	53.3	13	ADR47040	ADR47040	Dengue v
6	30.4	53.3	48	53.3	13	ADT48965	ADT48965	PCR prim
7	30.4	53.3	51	53.3	2	AAQ86123	AAQ86123	Primer HD
8	30.4	53.3	52	53.3	2	AAQ86204	AAQ86204	Sindbis/H
9	30.4	53.3	52	53.3	2	AAT31151	AAT31151	HDV rever
10	30.4	53.3	52	53.3	2	AAT30817	AAT30817	HDV riboz
11	30.4	53.3	52	53.3	2	AAV42334	AAV42334	Nested PC
12	30.4	53.3	52	53.3	2	AAV42426	AAV42426	Forward P
13	30.4	53.3	52	53.3	2	AAV60154	AAV60154	Nested PC
14	30.4	53.3	52	53.3	2	AAV60185	AAV60185	Reverse p
15	30.4	53.3	52	53.3	2	AAV70746	AAV70746	Reverse p
16	30.4	53.3	52	53.3	2	AAV70714	AAV70714	Nested pr
17	30.4	53.3	52	53.3	3	AAZ92930	AAZ92930	Hepatitis
18	30.4	53.3	52	53.3	3	AAZ92970	AAZ92970	Hepatitis
19	30.4	53.3	52	53.3	3	AAZ92843	AAZ92843	Hepatitis
20	30.4	53.3	52	53.3	3	AAZ92803	AAZ92803	Hepatitis


```

(PVSH ) UNIV SHERBROOKE.
Perreault J, Ananvoranich S, Lafontaine D;
WPI; 2000-096791/08.
New construction of nucleic acid enzyme useful for biotechnological,
diagnostic and therapeutic applications.
Example 1; Fig 2; 52pp; English.
This is the nucleotide sequence of a trans-acting antigenomic delta
ribozyme of the invention. This ribozyme cleaves substrate Sp1.1 (see
AAZ57641). The invention relates to a nucleic acid enzyme (e.g.
deltaZp1.1) that is constructed to have a substrate binding portion with
the following sequence 3'-UNNKN-5'. The substrate of the enzyme has the
sequence 5'-H'-GNHNN-3'. The binding portion of the enzyme (ribozyme)
base pairs to 6 nucleotides 3' to the cleavage site of the substrate
(cleavage site is represented by *). At least one nucleotide is present
5' to the cleavage site of the substrate sequence. The enzyme of the
invention is used to cleave a substrate nucleotide sequence at a specific
cleavage site by mixing the substrate with the enzyme. The enzyme is used
to cleave viral RNA or RNA causing for example an inherited disease. The
enzymes also have other therapeutic, biotechnological and diagnostic
applications. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
Query Match 83.2%; Score 47.4; DB 3; Length 57;
Best Local Similarity 78.9%; Pred. NO. 0.00032;
Matches 45; Conservative 6; Mismatches 6; Indels 0; Gaps 0
QY 1 GGGUCCACCUCGCGGNNNNNNNUGGCGCAUGGCGUUCGUGGCUAAGGACCC 57
DB 1 GGGUCCACCUCGCGGUCGCGACCGUGGCAUGGCGUUCGUGGCUAAGGACCC 57
RESULT 4
AAZ57639
ID ID AAZ57639 standard; RNA; 37 BP.
XX
AC AAZ57639;
XX
XX 05-APR-2000 (first entry)
XX
XX Nucleotide sequence of bimolecular ribozyme RZA fragment.
XX
XX Bimolecular ribozyme; viral RNA cleavage; RZA fragment;
XX inherited disease; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /*tag= a
FT /bound_moiety= "RzB fragment of bimolecular ribozyme"
FT /note= "Forms double-stranded region with bases 20-16 of
FT sequence AAZ57640"
FT
FT stem_loop 7..19
FT /*tag= b
FT /bound_moiety= "RzB fragment of bimolecular ribozyme"
FT /note= "Forms double-stranded region with bases 11-6 of
FT sequence AAZ57641"
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FT misc_binding 20..25
FT /*tag= c
FT /bound_moiety= "RzB fragment of bimolecular ribozyme"
FT /note= "Forms double-stranded region with bases 8-1 of
FT sequence AAZ57640"
FT
FT
XX
XX WO9955856-A2.
XX

```

```

XX
DR WPI; 2004-625870/60.
PT Virus-like particle vaccines containing dengue virus recombinant replicon
PT as core for carrier, applicable in preventives or/and remedies for tumors
PT like cervical cancer and viral diseases.
PS
XX Example 4; SEQ ID NO 37; 38pp; Chinese.
XX
CC A dengue virus recombinant replicon has a deletion of the complete coding
CC sequence for preM protein of dengue virus and also includes elements of
CC e.g. the non-coding region in the whole of the 5'-end, the coding region
CC of the front 20 amino acids in the C protein, and the coding region of
CC NS1 protein signal; coding regions of all non-structural proteins. The
CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to an oligonucleotide used in the
CC recombinant replicon of the invention.
XX
SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 53.3%; Score 30.4; DB 13; Length 48;
Best Local Similarity 59.4%; Pred. No. 75;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUCGCGGUNNNNNNUGGCGAUGC 35
Db 17 TCACCTCTCGCGGTCCGACCTGGGCATCCG 48

RESULT 6
ADT48965
XX ADT48965 standard; DNA; 48 BP.
AC ADT48965;
XX
XX 16-DEC-2004 (first entry)
DE PCR primer 5' HDVx, seq id 29.
XX
XX Viricide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;
KW PCR; primer; ss.
XX
OS Viruses.
XX
XX WO2004082712-A1.
PN
XX
XX 30-SEP-2004.
PD
XX
XX 19-MAR-2004; 2004WO-CN000232.
PF
XX
XX 20-MAR-2003; 2003CN-00115912.
PR
XX
XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA (TENG-) TENGGEN BIOMEDICAL CO.
PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX
XX Pang X;
XX
XX WPI; 2004-699719/68.
XX
XX Bivalent vaccines for preventing and treating Japanese (B) encephalitis
PT and hepatitis B produced by recombinant technique using encephalitis B
PT virus as vector to express antigen gene of hepatitis B.
PT

```

```

XX
PS Example 8; SEQ ID NO 29; 33pp; Chinese.
XX
CC The invention relates to a recombinant Japanese encephalitis B virus
CC constructed from encephalitis B virus and a recombinant genome, where the
CC genome is inserted with an exogenous nucleotide sequence for
CC recombination and capable of retaining its self-replication function. The
CC virus is useful in producing the bivalent vaccines for preventing and
CC treating Japanese (B) encephalitis and hepatitis B. Such vaccines are
CC producible at low cost and have high immunosensitivity, in which the
CC recombinant virus can efficiently express the antigen of hepatitis B
CC virus with the safety and immunogenicity of attenuated encephalitis B
CC virus vaccines. The current sequence represents a PCR primer used in an
CC example from the invention.
XX
SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 53.3%; Score 30.4; DB 13; Length 48;
Best Local Similarity 59.4%; Pred. No. 75;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUCGCGGUNNNNNNUGGCGAUGC 35
Db 17 TCACCTCTCGCGGTCCGACCTGGGCATCCG 48

RESULT 7
AAQ86173
ID AAQ86173 standard; DNA; 51 BP.
XX
XX AAQ86173;
XX
XX 25-MAR-2003 (revised)
DT 21-NOV-1995 (first entry)
XX
XX Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.
XX
XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
KW transcription initiation; non-structural protein; subgenomic fragment;
KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
KW primer; polymerase chain reaction; cystic fibrosis; ss.
XX
XX Synthetic.
XX
XX WO9507994-A2.
PN
XX
XX 23-MAR-1995.
PD
XX
XX 15-SEP-1994; 94WO-US010469.
PF
XX
XX 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR
XX
XX (VIAG-) VIAGENE INC.
PA
XX
XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
PI
XX
XX WPI; 1995-131362/17.
DR
XX
XX New alpha virus vectors for gene therapy - of viral infection, cancer,
PT auto-immune disease, etc., and as vaccines.
PT
XX
XX Example 2; Page 68; 260pp; English.
PS
XX
XX The sequences given in AAQ86167-81 are primers which were used in the
CC generation of plasmid DNA which initiates Sindbis infection. The
CC amplified DNA sequences were used in the construction of a eukaryotic
CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
CC comprise a 5' sequence capable of initiating transcription of an
CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
CC proteins, a viral junction region which has been inactivated such that
CC viral transcription of the subgenomic fragment is prevented, and an
CC alphavirus RNA polymerase recognition sequence. Inactivation of the viral
CC

```

CC junction region prevents transcription of the subgenomic fragment making
 CC vectors such as this suitable for a wide variety of applications, eg.
 CC gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 53.3%; Score 30.4; DB 2; Length 51;
 Best Local Similarity 59.4%; Pred. No. 76;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNNUGGCAUCCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 8
 AAQ86204
 ID AAQ86204 standard; DNA; 52 BP.

XX AC AAQ86204;
 XX 25-MAR-2003 (revised)
 DT 23-NOV-1995 (first entry)
 XX
 DE Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.
 XX
 KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX
 OS Synthetic.

XX
 PN WO9507994-A2.
 XX
 PD 23-MAR-1995.

XX 15-SEP-1994; 94WO-US010469.
 XX 15-SEP-1993; 93US-0012791.
 PR 18-FEB-1994; 94US-00198450.

XX (VIAG-) VIAGENE INC.

XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
 WPI; 1995-131362/17.

XX New alpha virus vectors for gene therapy - of viral infection, cancer,
 PT auto-immune disease, etc., and as vaccines.

XX Example 7; Page 114; 260pp; English.

XX The sequences given in AAQ86200-15 are primers which were used in the
 CC production of alphavirus vectors expressing multiple heterologous genes.
 CC These vectors are eukaryotic layered vector initiation systems (ELVIS)
 CC derived from Sindbis. ELVIS's comprise a 5' sequence capable of
 CC initiating transcription of an alphavirus, a nucleotide sequence encoding
 CC alphavirus non-structural proteins, a viral junction region which has
 CC been inactivated such that viral transcription of the subgenomic fragment
 CC is prevented, and an alphavirus RNA polymerase recognition sequence.
 CC Inactivation of the viral junction region prevents transcription of the
 CC subgenomic fragment making vectors such as this suitable for a wide
 CC variety of applications, eg. gene therapy for the treatment of cystic
 CC fibrosis. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 53.3%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 76;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNNUGGCAUCCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 9
 AAT31151
 ID AAT31151 standard; DNA; 52 BP.

XX AC AAT31151;
 XX 12-SEP-1996 (first entry)
 DT HDV reverse primer HDV17-68.
 XX
 DE Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
 KW polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;
 KW ribozyme; ss.

XX Synthetic.

XX WO9617072-A2.

XX 06-JUN-1996.

XX 30-NOV-1995; 95WO-US015490.

XX 30-NOV-1994; 94US-00348472.

PR 18-JAN-1995; 95US-00376184.

PR 15-MAR-1995; 95US-00405827.

XX (CHIR) CHIRON VIAGENE INC.

XX Dubensky TW, Polo JM, Ibanez CE, Chang SM, Jolly DJ, Driver DA;

PI Belli BA;

XX WPI; 1996-277785/28.

XX New recombinant alpha-virus vectors - used to develop prods and methods
 PT for use in gene therapy and in the prodn. of vaccines.

XX Example 7; Page 120; 256pp; English.

XX Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)
 CC nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)
 CC for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV
 CC (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment
 CC contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping
 CC synthesis is used in a second round of PCR using primers HDV49-XC and
 CC SIN276-SPE. The resulting construct contains the expression cassette
 CC elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction
 CC region/Sindbis structural protein genes/Sindbis 3'-end untranslated
 CC region, designated pds'26s. This was inserted into pCDNA3. Packaging cell
 CC line cassettes were constructed that allow inducible expression of
 CC structural proteins via alphavirus vectors

XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 53.3%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 76;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNNUGGCAUCCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 10
 AAT30817

ID AAT30817 standard; DNA; 52 BP.

XX AAT30817;

```

DT 12-SEP-1996 (first entry)
XX HDV ribozyme primer HDV17-68.
XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;
KW polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;
KW hepatitis delta virus; ss.
XX Synthetic.
XX WO9617072-A2.
XX 06-JUN-1996.
XX 30-NOV-1995; 95WO-US015490.
XX 30-NOV-1994; 94US-00348472.
XX 18-JAN-1995; 95US-00376184.
XX 15-MAR-1995; 95US-00405827.
XX (CHIR ) CHIRON VIAGENE INC.
XX Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;
PI Belli BA;
XX WPI; 1996-277785/28.
XX New recombinant alpha-virus vectors - used to develop prods and methods
PT for use in gene therapy and in the prodn. of vaccines.
XX Example 3; Page 85; 256pp; English.
XX Primer SHDV1F (AAAT30816) contains a buffer sequence allowing enzyme
CC digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme
CC sequence. It was used with nested primer HDV17-68 (AAAT30817) and reverse
CC primer SHDV84R (AAAT30818) to generate an HDV ribozyme. This antigenomic
CC ribozyme can be placed between the polyA tract at the 3' end of a Sindbis
CC virus-based eukaryotic layered vector initiation system, ELVIS, and the
CC transcription terminal signals to produce alphavirus expression vectors
CC useful in methods of gene therapy and for vaccine prodn
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
SQ
Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGGTCGACCTGGGCATCCG 32
RESULT 11
AAV42394
ID AAV42394 standard; DNA; 52 BP.
XX
XX AAV42394;
AC AAV42394;
XX
XX 02-OCT-1998 (first entry)
XX
XX Nested PCR primer HDV17-68 of the invention.
DE
XX DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; PCR primer; ss.
XX Synthetic.
XX US5789245-A.
XX 04-AUG-1998.
XX
XX 30-OCT-1996; 96US-00741881.
XX

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PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX (CHIR ) CHIRON CORP.
PA Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX WPI; 1998-446089/38.
XX
XX DNA alpha:virus structural protein expression cassettes - for producing
PT recombinant alpha:virus particles.
XX Example 3; Col 69; 140pp; English.
XX PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC invention. The specification describes a DNA alphavirus structural
CC protein expression cassette which comprises an inducible promoter and an
CC alphavirus structural protein gene, where the promoter directs the
CC expression of the alphavirus structural protein gene upon induction of
CC the promoter within a cell, and where prior to induction within the cell,
CC the expression cassette does not express sufficient quantities of
CC structural proteins to be cytotoxic to a BHK cell containing the
CC expression cassette. The products may be used to inhibit pathogens and
CC stimulate an immune response
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
SQ
Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGGTCGACCTGGGCATCCG 32
RESULT 12
AAV42426
ID AAV42426 standard; DNA; 52 BP.
XX
XX AAV42426;
AC AAV42426;
XX
XX 02-OCT-1998 (first entry)
XX
XX Forward PCR primer HDV17-68.
DE
XX DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; PCR primer; ss.
XX Synthetic.
XX US5789245-A.
XX 04-AUG-1998.
XX
XX 30-OCT-1996; 96US-00741881.
XX
XX 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX (CHIR ) CHIRON CORP.
PA Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX WPI; 1998-446089/38.
XX
XX DNA alpha:virus structural protein expression cassettes - for producing
PT

```


PT recombinant alpha:virus particles.
 XX Example 7; Col 103; 140pp; English.
 CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and an
 CC alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the cell,
 CC the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 53.3%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 76;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUGCGGCGGNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||: ||
 Db 1 TCACCTCTCGCGGTCCGACCTGGGCAATCCG 32
 RESULT 13
 AAV60154
 ID AAV60154 standard; DNA; 52 BP.
 XX
 AC AAV60154;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 DE Nested PCR primer HDV17-68.
 XX
 KW Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 OS Synthetic.
 OS Hepatitis D virus.
 XX
 PN US5814482-A.
 XX
 PD 29-SEP-1998.
 XX
 PF 30-OCT-1996; 96US-00739158.
 XX
 PR 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 10-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 PA (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 XX
 DR WPI; 1998-541753/46.
 XX
 PT Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 PS Example 3; Col 71-72; 144pp; English.
 XX
 CC PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
 CC ribozyme sequence. The product is used in the course of the invention.

CC The specification describes an eukaryotic layered vector initiation
 CC system, based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
 CC The RNA comprises a vector construct which autonomously amplifies in the
 CC cell and expresses a heterologous nucleic acid sequence which encodes an
 CC antigen or modified form that stimulates an immune response within an
 CC animal. The system is useful for stimulating an immune response to an
 CC antigen by introducing the vector into target cells, preferably by
 CC infection in vivo, especially where the immune response is a cell
 CC mediated, HLA class I-restricted or an HLA class II-restricted immune
 CC response. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 53.3%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 76;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUGCGGCGGNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||: ||
 Db 1 TCACCTCTCGCGGTCCGACCTGGGCAATCCG 32
 RESULT 14
 AAV60185
 ID AAV60185 standard; DNA; 52 BP.
 XX
 AC AAV60185;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 DE Reverse PCR primer HDV17-68.
 XX
 KW Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 OS Synthetic.
 XX
 PN US5814482-A.
 XX
 PD 29-SEP-1998.
 XX
 PF 30-OCT-1996; 96US-00739158.
 XX
 PR 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 PA (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 XX
 DR WPI; 1998-541753/46.
 XX
 PT Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 PS Example 5; Col 108; 144pp; English.
 XX
 CC PCR primers AAV60184-85 are used in the course of the invention. The
 CC specification describes an eukaryotic layered vector initiation system,
 CC based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.

CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGUNNNNNNUGGCGAUGCG 35
:||||:||||:||||:||||:||||:||||: ||
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15
AAV70746
ID AAV70746 standard; DNA; 52 BP.
XX
AC AAV70746;
XX
DT 20-MAR-2003 (revised)
DT 02-FEB-1999 (first entry)
XX
DE Reverse PCR primer HDV17-68 used to amplify Hepatitis delta virus.
XX
KW Alphavirus vector construct; gene therapy; PCR primer; ss.
XX
OS Synthetic.
OS Hepatitis D virus.
XX
PN US5843723-A.
XX
PD 01-DEC-1998.
XX
PF 30-OCT-1996; 96US-00739167.
XX
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chang SMW, Jolly DJ, Dubeney TW, Belli BA, Ibanez CE, Driver DA;
PI Polo JM;
XX
DR WPI; 1999-044581/04.
XX
PT Alphavirus vectors constructs containing a 5' promoter of viral cDNA by
PT in vitro transcription - used in gene therapy.
XX
PS Example 7; Col 103; 140pp; English.
XX
CC PCR primers AAV70745-46 are used to amplify part of the hepatitis delta
CC virus (HDV) genome. The amplified product is used in the production of
CC the alphavirus vector constructs of the invention. These constructs
CC comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA
CC from the viral cDNA by in vitro transcription, followed by a 5' sequence
CC which initiates transcription of alphavirus RNA, followed by a nucleotide
CC sequence encoding alphavirus nonstructural proteins, a viral junction
CC region which has been inactivated such that viral transcription of a
CC subgenomic fragment is prevented, an internal ribosome entry site or a
CC sequence which promotes ribosome read through between adjacent reading
CC frames, and an alphavirus RNA polymerase recognition sequence. The
CC recombinant alphavirus vectors can be used for gene therapy. (Updated on
CC 20-MAR-2003 to correct PR field.)

XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGUNNNNNNUGGCGAUGCG 35
:||||:||||:||||:||||:||||:||||: ||
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

Search completed: March 15, 2005, 16:13:00
Job time : 319.25 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:26:58 ; Search time 94.75 Seconds
(without alignments)
984.356 Million cell updates/sec

Title: US-09-699-667E-61
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Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	30.4	53.3	52	1	US-08-741-881-80
3	30.4	53.3	52	1	US-08-739-158-40
4	30.4	53.3	52	1	US-08-739-158-80
5	30.4	53.3	52	2	US-08-739-167-40
6	30.4	53.3	52	2	US-08-739-167-80
7	30.4	53.3	52	3	US-08-404-796-40
8	30.4	53.3	52	3	US-08-404-796-80
9	30.4	53.3	52	3	US-08-931-869-40
10	30.4	53.3	52	3	US-08-931-869-80
11	30.4	53.3	52	3	US-09-350-399-40
12	30.4	53.3	52	3	US-09-350-399-80
13	30.4	53.3	52	3	US-09-236-140A-40
14	30.4	53.3	52	3	US-09-236-140A-80
15	29	50.9	56	3	US-09-415-784-39
16	29	50.9	56	3	US-09-415-785A-39
17	29	50.9	56	3	US-08-944-465-39
18	29	50.9	56	3	US-09-415-868-39
19	29	50.9	56	3	US-09-415-900-39
20	29	50.9	56	4	US-09-507-362-39
21	24	42.1	52	1	US-08-238-963A-19
C 22	23.2	40.7	47	4	US-09-422-978-3088
C 23	23	40.4	58	3	US-08-646-695-40
C 24	23	40.4	58	5	PCT-US96-06053-40
25	22.4	39.3	39	3	US-08-485-3558-7
26	22	38.6	45	3	US-08-978-806-3
27	22	38.6	45	2	US-08-632-882-5

28	22	38.6	45	4	US-09-419-125-5	Sequence 5, Appli
29	22	38.6	49	1	US-08-758-306-6	Sequence 6, Appli
30	22	38.6	49	3	US-08-985-162-1875	Sequence 1875, Ap
31	22	38.6	49	3	US-08-998-099-373	Sequence 373, App
32	22	38.6	49	3	US-09-112-086B-7	Sequence 7, Appli
33	22	38.6	49	3	US-08-975-238-5	Sequence 5, Appli
34	22	38.6	49	3	US-09-094-381C-18	Sequence 18, Appl
35	22	38.6	49	3	US-08-679-645-1234	Sequence 1234, Ap
36	22	38.6	49	3	US-09-676-807-9	Sequence 9, Appli
37	22	38.6	49	4	US-09-216-584-38	Sequence 38, Appl
38	22	38.6	49	4	US-09-812-186-5	Sequence 5, Appli
39	22	38.6	49	4	US-09-401-063-1875	Sequence 1875, Ap
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41	21.4	37.5	57	1	US-08-120-827-52	Sequence 52, Appl
42	21.4	37.5	57	1	US-08-478-675-52	Sequence 52, Appl
43	21.2	37.2	34	3	US-08-974-549A-482	Sequence 482, App
44	21.2	37.2	34	4	US-08-912-951-249	Sequence 249, App
45	21.2	37.2	34	4	US-09-402-181B-482	Sequence 482, App

ALIGNMENTS

RESULT 1
US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

Query Match 53.3%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNNUGGCAUGCG 35

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-40

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCGAUGC 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 8

US-08-404-796-80
Sequence 80, Application US/08404796
Patent No. 6015686
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 15-MAR-1995
APPLICATION NUMBER: US/08/404,796
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-404-796-80

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCGAUGC 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 9

US-08-931-869-40
Sequence 40, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-SEP-1997
APPLICATION NUMBER: US/08/931,869
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 15-MAR-1995
APPLICATION NUMBER: US 08/404,796
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-40

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCGAUGC 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 10

US-08-931-869-80
Sequence 80, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:

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; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-931-869-80

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 1; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGNNNNNUGGCGAUCG 35
Db 1 TCCACCTCTCGCGGTCGCGACCTGGGCATCCG 32

RESULT 11
US-09-350-399-40
; Sequence 40, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
; US-09-350-399-40

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 1; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGNNNNNUGGCGAUCG 35
Db 1 TCCACCTCTCGCGGTCGCGACCTGGGCATCCG 32

RESULT 12
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
; US-09-350-399-80
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Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 13

US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-236-140A-40

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 14

US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; Polo, John M.
; Ibanez, Carlos E.

Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15

US-09-415-784-39
; Sequence 39, Application US/09415784
; Patent No. 6391632
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/415,784
FILING DATE: 08-Oct-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-415-784-39

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Best Local Similarity 58.6%; Pred. No. 25;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
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Db 27 TCCACCTCTCTCGCGGTCCGACCTGGGCAT 55

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GenCore version 5.1.6
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Title: US-09-699-667E-61
Perfect score: 57
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30.4	53.3	52	17	US-10-346-880-80 Sequence 80, Appl
3	30.4	53.3	52	17	US-10-150-407-40 Sequence 40, Appl
4	30.4	53.3	52	17	US-10-150-407-80 Sequence 80, Appl
5	29	50.9	56	17	US-09-507-362-39 Sequence 39, Appl
6	25.8	44.3	56	17	US-10-391-441-39 Sequence 6071, Ap
7	25.8	44.3	60	10	US-09-908-975-6071 Sequence 13039, A
8	25.6	45.9	60	10	US-09-908-975-13039 Sequence 10, Appl
9	24	42.1	47	17	US-10-380-438-10 Sequence 10629, A
10	24	42.1	60	10	US-09-908-975-10629 Sequence 20125, A
11	24	42.1	60	10	US-09-908-975-20125

c	12	23.2	40.7	47	17	US-10-349-143-3088 Sequence 3088, Ap
c	13	23	40.4	60	10	US-09-908-975-22269 Sequence 22269, A
c	14	22.6	39.6	60	10	US-09-908-975-23713 Sequence 23713, A
c	15	22.4	39.3	25	19	US-10-719-900-864120 Sequence 864120,
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c	18	22	38.6	33	10	US-09-864-636A-381 Sequence 381, App
c	19	22	38.6	33	10	US-09-864-636A-382 Sequence 382, App
c	20	22	38.6	33	11	US-09-864-426A-381 Sequence 381, App
c	21	22	38.6	33	11	US-09-864-426A-382 Sequence 382, App
c	22	22	38.6	33	16	US-10-084-839-381 Sequence 381, App
c	23	22	38.6	33	16	US-10-084-839-382 Sequence 382, App
c	24	22	38.6	39	8	US-08-978-806-3 Sequence 3, Appli
c	25	22	38.6	39	9	US-09-972-834-3 Sequence 3, Appli
c	26	22	38.6	49	9	US-09-812-186-5 Sequence 5, Appli
c	27	22	38.6	49	10	US-09-961-077-1234 Sequence 1234, Ap
c	28	22	38.6	49	13	US-10-103-480-9 Sequence 9, Appli
c	29	22	38.6	49	15	US-10-156-433-38 Sequence 38, Appl
c	30	22	38.6	49	16	US-10-112-814-38 Sequence 38, Appl
c	31	21.8	38.2	47	18	US-10-343-514-58 Sequence 58, Appl
c	32	21.8	38.2	47	18	US-10-343-514-72 Sequence 72, Appl
c	33	21.8	38.2	51	18	US-10-813-638-704 Sequence 704, App
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c	35	21.6	37.9	44	18	US-10-851-383-226 Sequence 226, App
c	36	21.6	37.9	44	18	US-10-851-383-336 Sequence 336, App
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c	39	21.6	37.9	60	10	US-09-908-975-18877 Sequence 18877, A
c	40	21.4	37.5	41	17	US-10-035-833A-915 Sequence 915, App
c	41	21.4	37.5	41	17	US-10-035-833A-9223 Sequence 9223, Ap
c	42	21.4	37.5	51	17	US-10-393-815-80 Sequence 80, Appl
c	43	21.2	37.2	34	14	US-10-044-692-249 Sequence 249, App
c	44	21.2	37.2	34	15	US-10-044-539-249 Sequence 249, App
c	45	21.2	37.2	34	17	US-10-325-810-482 Sequence 482, App

ALIGNMENTS

RESULT 1
US-10-346-880-40
; Sequence 40, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0


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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-507-362-39

Query Match 50.9%; Score 29; DB 10; Length 56;
Best Local Similarity 58.6%; Pred. No. 84;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCGCGGGUNNNNNNUGGCGCAU 32
DB 27 TCCACCTCTCGCGTCCGACCTGGCAT 55

RESULT 6
US-10-391-441-39
; Sequence 39, Application US/10391441
; Publication No. US20030232058A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; POLO, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frollov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391.441
; FILING DATE: 17-Mar-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/507.362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match 50.9%; Score 29; DB 17; Length 56;
Best Local Similarity 58.6%; Pred. No. 84;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCGCGGGUNNNNNNUGGCGCAU 32
DB 27 TCCACCTCTCGCGTCCGACCTGGCAT 55

```

RESULT 7
US-09-908-975-6071/c
; Sequence 6071, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6071
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-6071

Query Match 45.3%; Score 25.8; DB 10; Length 60;
Best Local Similarity 46.7%; Pred. No. 1e+03;
Matches 21; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY 3 GUCCACUCCUGCGGNNNNNUGGCGCAUGCGGUCCGCAUGGC 47
DB 46 GTCCAGCTCTCGGCTCTCGATGCGCGGATCTGCACCGC 2

RESULT 8
US-09-908-975-13039/c
; Sequence 13039, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13039
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-13039

Query Match 44.9%; Score 25.6; DB 10; Length 60;
Best Local Similarity 45.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 6 CACCUCCUGCGGNNNNNUGGCGCAUGCGGUCCGCAUG 45
DB 53 CACGTCCTTGAGGTGCTGCATATGCGTGGGATGAGCATG 14

RESULT 9
US-10-380-438-10
; Sequence 10, Application US/10380438
; Publication No. US20040053829A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; TITLE OF INVENTION: FUSION PROTEIN FROM ANTIBODY CYTOKINE-CYTOKINE INHIBITOR (SELECTOR;
; FILE REFERENCE: MBP-020XX
; CURRENT APPLICATION NUMBER: US/10/380,438
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: DE 100 45 592.1
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Primer 1 for
; OTHER INFORMATION: the amplification of the trimerization of chicken tenascin
US-10-380-438-10

Query Match 42.1%; Score 24; DB 17; Length 47;
Best Local Similarity 52.5%; Pred. No. 4e+03;
Matches 21; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
QY 1 GGUCCACUCCUGCGGNNNNNUGGCGCAUGCGGUUC 40
DB 8 GGGCCACAGCAGCGCGCGCTGTGCTGTGCGGCTGC 47

RESULT 10
US-09-908-975-10629/c
; Sequence 10629, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10629
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-10629

Query Match 42.1%; Score 24; DB 10; Length 60;
Best Local Similarity 45.0%; Pred. No. 4.1e+03;
Matches 18; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
QY 4 UCCACUCCUGCGGNNNNNUGGCGCAUGCGGUUCGCA 43
DB 43 TCTACTGCTCGGACAATGGTGTCCATGCTGCTTTGCA 4

RESULT 11
US-09-908-975-20125
; Sequence 20125, Application US/09908975
; Publication No. US20030165843A1

GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20125
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-20125

Query Match 42.1%; Score 24; DB 10; Length 60;
Best Local Similarity 45.0%; Pred. No. 4.1e+03;
Matches 18; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
QY 4 UCCACCUCCUGCGGUNNNNUGGCAUGCGGCUUCGCA 43
Db 17 TCCTCTCAACTCGGTCAACGCTGGGGCTTCTGCTTCGCA 56

RESULT 12
US-10-349-143-3088/c
Sequence 3088, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR FILING DATE: US/09/422,978
PRIOR APPLICATION NUMBER: 1999-10-20
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 3088
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-22706-367 : polymorphic base T or C
US-10-349-143-3088

Query Match 40.7%; Score 23.2; DB 17; Length 47;
Best Local Similarity 38.6%; Pred. No. 7.4e+03;
Matches 17; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 2 GGUCCACCUCCUGCGGUNNNNUGGCAUGCGGCUUCGCAUG 45
Db 44 GGTCCTCATCATCACTGCAAGTGGGCATTTCTTACTTCATG 1

RESULT 13

US-09-908-975-22269
Sequence 22269, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22269
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-22269

Query Match 40.4%; Score 23; DB 10; Length 60;
Best Local Similarity 41.0%; Pred. No. 8.9e+03;
Matches 16; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
QY 2 GGUCCACCUCCUGCGGUNNNNUGGCAUGCGGCUUC 40
Db 15 GGTCCACATCATCAAGCTTCATGCTTTGCTCCTCGGGTTC 53

RESULT 14
US-09-908-975-23713/c
Sequence 23713, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23713
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-23713

Query Match 39.6%; Score 22.6; DB 10; Length 60;
Best Local Similarity 39.6%; Pred. No. 1.2e+04;
Matches 21; Conservative 13; Mismatches 19; Indels 0; Gaps 0;
QY 1 GGUCCACCUCCUGCGGUNNNNUGGCAUGCGGCUUCGCAUGCGCUAAGG 53
Db 55 GGATCAGCTACTGGGGTTGGCACGTTGTATGTAGCTGCAATACGAAGGAG 3

RESULT 15
US-10-719-900-864120

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:20:59 ; Search time 2293 Seconds
(without alignments)
946.212 Million cell updates/sec

Title: US-09-699-667E-61
Perfect score: 57
Sequence: 1 ggguccaccuccggun.....uucgauggcuaggagacc 57

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25.4	44.6	49	1	AI956143 wt35601.x
C 2	23.6	41.4	49	1	AA878748 of85b02.s
C 3	23.6	41.4	56	8	BH638481 1008022G0
C 4	23.6	41.4	57	7	R10187 yf35d03.r1
C 5	23.2	40.7	54	6	CB058194 NISC_jx01
C 6	23.4	40.6	58	8	AZ385410 IM0143E22
C 7	22.8	38.6	55	1	AA232965 zr69a04.s
C 8	22.8	38.6	55	9	AL944166 Arabidops
C 9	21.6	37.9	53	1	AI906698 QV-Brl23-
C 10	21.6	37.9	58	9	CR360020 Arabidops
C 11	21.4	37.5	42	4	BH830168 603072810
C 12	21.4	37.5	49	7	H23825 yn71e03.s1
C 13	21.4	37.5	57	9	CL234247 02S0288-0
C 14	21.2	37.2	42	7	CF316536 HD--05-N1
C 15	21.2	37.2	55	1	AA261309 vb03f02.r
C 16	21.2	37.2	55	8	BH903452 SALK_1026
C 17	21.2	37.2	55	8	BH903454 SALK_1026
C 18	21.2	37.2	55	8	BH903457 SALK_1026
C 19	21.2	36.8	31	1	AI688077 wa83d03.x
C 20	21.2	36.8	46	1	AA770617 oe54d02.s
C 21	21.2	36.8	50	9	CR021509 Reverse.s
C 22	21.2	36.8	60	1	AA762539 vv80a11.r
C 23	20.8	36.5	43	9	CG774833 1123021A1
C 24	20.8	36.5	46	1	AI937668 wp82b01.x

C	25	20.8	36.5	50	1	AIU102849
	26	20.8	36.5	51	2	BF583696 602096712
	27	20.8	36.5	52	4	BI692727 603343394
C	28	20.8	36.5	54	5	BQ567053 gi76d12.y
	29	20.8	36.5	57	9	CR229172 Reverse.s
C	30	20.8	36.5	58	8	BH803980 1008106H0
C	31	20.6	36.1	38	4	BI760995 603048518
C	32	20.6	36.1	45	8	AZ656574 IM0532012
C	33	20.6	36.1	46	4	BI517548 603041841
C	34	20.6	36.1	50	1	AIU104320
C	35	20.6	36.1	50	1	AIU104848
C	36	20.6	36.1	54	1	AA428670 zv50b11.r
C	37	20.6	36.1	58	1	AI623494 ts19e02.x
C	38	20.6	36.1	60	4	BG919968 602823314
C	39	20.6	36.1	60	6	CD952940 SBF_142_G
C	40	20.4	35.8	47	9	AJ599744 Arabidops
C	41	20.4	35.8	48	8	AZ480319 IM0301C16
C	42	20.4	35.8	49	8	AZ448959 IM0247A04
C	43	20.4	35.8	50	1	AIU104140
C	44	20.4	35.8	50	1	AIU106765
C	45	20.4	35.8	52	1	AI745373 tr22d12.x

ALIGNMENTS

RESULT 1
AI956143/c 49 bp mRNA linear EST 19-AUG-1999
LOCUS wt35601.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2509464 3'
DEFINITION similar to TR:Q61402 Q61402 GRANULE CELL ANTISERUM POSITIVE 8 ;
mRNA sequence.
ACCESSION AI956143 GI:5748453
VERSION AI956143.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2509464"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; Salt;
Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life technologies catalog #:
11548-013"

ORIGIN

Query Match 44.6%; Score 25.4; DB 1; Length 49;
Best Local Similarity 46.5%; Pred. Mismatches 11; Indels 0; Gaps 0;
Matches 20; Conservative 12; Matches 11; Indels 0; Gaps 0;


```

DEFINITION 02S0288-04D1-A12 UniformMu MuTAIL Library Zea mays genomic clone
ACCESSION 02S0288-04D1-A12, genomic survey sequence.
VERSION CU234247
KEYWORDS CU234247.1 GI:40778227
SOURCE GSS.
ORGANISM Zea mays
           Zea mays
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 57)
AUTHORS Latschaw S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize
        population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
        Plant Molecular and Cellular Biology Program
        University of Florida
        PO 110690 Gainesville, FL 32611-0690, USA
        Tel: 352-392-1928 x322
        Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
02S0288-04, Primer set: D
Class: transposon insertion site.
FEATURES
    source
    1..57
    Location/Qualifiers
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="W22 (ACR, bz1-m9)"
        /cultivar="UniformMu"
        /db_xref="taxon:4577"
        /clone="02S0288-04D1-A12"
        /notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
        insertions in Mu inactive lines were extracted from the
        UniformMu maize population by the thermo asymmetric
        interlaced PCR (TAIL) protocol using primers specific for
        the Mu terminal inverted repeat and a set of 16 arbitrary
        primers. Amplicons were size enriched using Sepharose 400
        spin columns and cloned into the TOPO PCR4 vector."
ORIGIN
    Query Match 37.5%; Score 21.4; DB 9; Length 57;
    Best Local Similarity 51.6%; Pred. No. 5.8e+05;
    Matches 16; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCACUCCUCCGCGGUNNNNUGGCAUGCG 35
    ||| | | | | | | | | | | | | | | | | | | |
Db 11 CCAGCAGCTTGGCGGAGTGCGACTGCGCATGCG 41

RESULT 14
CF316536 42 bp mRNA linear EST 15-AUG-2003
LOCUS HD--05-N19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-N19, mRNA sequence.
ACCESSION CF316536
VERSION CF316536.1 GI:33688297
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim, J.S., Jun, K.M., Cheong, F.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
        Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
        of Bioscience and Bioinformatics, Myongji University

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
    1..42
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="HD--05-N19"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 2 weeks"
    /lab_host="E.coli DH10B"
    /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
    cDNA library (HD)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
    treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
    reverse transcribed and then used for PCR. mRNA was
    derived from rice Histone Deacetylase overexpression
    line."
ORIGIN
    Query Match 37.2%; Score 21.2; DB 7; Length 42;
    Best Local Similarity 38.1%; Pred. No. 6.5e+05;
    Matches 16; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 7 ACCUCCUCCGCGGUNNNNUGGCAUGCGCUUCGCAUGCGU 48
    ||| | | | | | | | | | | | | | | | | | | |
Db 1 AACTCCACGAGTTGAAGCTGTCTTGCCTGCACTGCAATGCCT 42

RESULT 15
AA261309 55 bp mRNA linear EST 18-MAR-1997
LOCUS vb03f02.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:747867 5'
DEFINITION similar to SW:GAMT_RAT P10868 GUANIDINOACETATE N-METHYLTRANSFERASE
        ; mRNA sequence.
ACCESSION AA261309
VERSION AA261309.1 GI:1895853
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 55)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
        Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
        Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
        Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
        Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
        WashU-HMI Mouse EST Project
        Washington University School
        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
        Tel: 314 286 1800
        Fax: 314 286 1810
        Email: mouseest@watson.wustl.edu
        This clone is available royalty-free through LNL ; contact the
        IMAGE Consortium (info@image.lnl.gov) for further information.
        MGI:456851
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28mi3 rev2 ET from Amersham
High quality sequence stop: 1.
        Location/Qualifiers
            1..55
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /clone="IMAGE:747867"

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/tissue type="Liver"
/lab_host="DH10B"
/clone_lib="Soares mouse NML"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGAATCTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
```

ORIGIN

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Query Match      37.2%; Score 21.2; DB 1; Length 55;
Best Local Similarity 47.6%; Pred. No. 6.6e+05;
Matches 20; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      16  CGGUNNNNNNUGGCGCAUGCGGCUUCGCAUGGCUAAGGACCC 57
      || :::: || :||| ||| :||| :|||
Db      13  CGGCGCGGCGAGGACTGCGGCCCCCGGTGGCTCGGCGCCCC 54
```

Search completed: March 15, 2005, 20:38:02
Job time : 2306 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C	1	57	100.0	57	6	AX012282 Sequence
	2	57	100.0	57	6	AX012283 Sequence
	3	57	100.0	57	6	AX012285 Sequence
	4	57	100.0	57	6	AX012286 Sequence
	5	57	100.0	57	6	AX012287 Sequence
	6	57	100.0	57	6	AX012288 Sequence
	7	57	100.0	57	6	AX012289 Sequence
	8	57	100.0	57	6	AX012290 Sequence
	9	47.4	83.2	57	6	AX012284 Sequence
C	10	37	64.9	37	6	AX012291 Sequence
	11	32.2	56.5	168545	9	AX012291 Sequence
	12	31.8	55.8	61	6	AL1390 Sequence 18
C	13	31.2	54.7	219811	2	AC034123 Mus muscu
	14	31.2	54.7	255261	10	AL929212 Mouse DNA
	15	30.6	53.7	159423	9	AC008429 Homo sapi
C	16	30.6	53.7	174035	10	AC119266 Mus muscu
	17	30.6	53.7	186238	2	AC084828 Mus muscu
	18	30.6	53.7	197660	10	AL589650 Mouse DNA
	19	30.6	53.7	198304	2	AC117632 Mus muscu
	20	30.6	53.7	198304	2	AC117632 Mus muscu

```
other sequences; artificial sequences.
1
AUTHORS
  Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
  Nucleic acid enzyme for rna cleavage
JOURNAL
  Patent: WO 9955856-A 45 04-NOV-1999;
  ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
  PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="synthetic nucleic acid"
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  Query Match      100.0%; Score 57; DB 6; Length 57;
  Best Local Similarity 71.9%; Pred. No. 2.3e-05;
  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGAUGCGCUUCGCAUGGCUAAGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  Db 1 GGGTCCACCTCTCGCGGTCCGCCCTCGGCATCGCGCTTCGCATGGCTAAGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 3
AX012285
LOCUS
  AX012285
DEFINITION
  Sequence 47 from Patent WO9955856.
ACCESSION
  AX012285.1
VERSION
  AX012285.1 GI:9998346
KEYWORDS
  .
SOURCE
  synthetic construct
  other sequences; artificial sequences.
ORGANISM
  Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  Nucleic acid enzyme for rna cleavage
  Patent: WO 9955856-A 47 04-NOV-1999;
  ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
  PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
  source
    Location/Qualifiers
      1..57
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="synthetic nucleic acid"
ORIGIN
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  Best Local Similarity 71.9%; Pred. No. 2.3e-05;
  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGAUGCGCUUCGCAUGGCUAAGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  Db 1 GGGTCCACCTCTCGCGGTCCGCCCTCGGCATCGCGCTTCGCATGGCTAAGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 4
AX012286
LOCUS
  AX012286
DEFINITION
  Sequence 48 from Patent WO9955856.
ACCESSION
  AX012286
VERSION
  AX012286.1 GI:9998347
KEYWORDS
  .
SOURCE
  synthetic construct
  other sequences; artificial sequences.
ORGANISM
  Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  Nucleic acid enzyme for rna cleavage
  Patent: WO 9955856-A 48 04-NOV-1999;
  ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
  PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="synthetic nucleic acid"
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  Best Local Similarity 71.9%; Pred. No. 2.3e-05;
  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGAUGCGCUUCGCAUGGCUAAGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  Db 1 GGGTCCACCTCTCGCGGTCCGCCCTCGGCATCGCGCTTCGCATGGCTAAGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 5
AX012287
LOCUS
  AX012287
DEFINITION
  Sequence 49 from Patent WO9955856.
ACCESSION
  AX012287
VERSION
  AX012287.1 GI:9998348
KEYWORDS
  .
SOURCE
  synthetic construct
  other sequences; artificial sequences.
ORGANISM
  Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  Nucleic acid enzyme for rna cleavage
  Patent: WO 9955856-A 49 04-NOV-1999;
  ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
  PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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        /db_xref="taxon:32630"
        /note="synthetic nucleic acid"
ORIGIN
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  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
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  Db 1 GGGTCCACCTCTCGCGGTCCGCCCTCGGCATCGCGCTTCGCATGGCTAAGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 6
AX012288
LOCUS
  AX012288
DEFINITION
  Sequence 50 from Patent WO9955856.
ACCESSION
  AX012288
VERSION
  AX012288.1 GI:9998349
KEYWORDS
  .
SOURCE
  synthetic construct
  other sequences; artificial sequences.
ORGANISM
  Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  Nucleic acid enzyme for rna cleavage
  Patent: WO 9955856-A 50 04-NOV-1999;
  ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
  PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
  source
    Location/Qualifiers
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Query Match      100.0%; Score 57; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 2.3e-05;
Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGGCAUGCGCUUGCGCAUGGAGGACCC 57
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DB 1 GGGTCCACCTCTCGCGGTCGCACTGGGCATCGCGCTTCGCATGCTGAAGGACCC 57

RESULT 7
LOCUS AX012289 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION AX012289
VERSION AX012289.1 GI:9998350
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"

ORIGIN
Query Match      100.0%; Score 57; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 2.3e-05;
Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGGCAUGCGCUUGCGCAUGGAGGACCC 57
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DB 1 GGGTCCACCTCTCGCGGTCGCACTGGGCATCGCGCTTCGCATGCTGAAGGACCC 57

RESULT 8
LOCUS AX012290 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION AX012290
VERSION AX012290.1 GI:9998351
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 52 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"

ORIGIN
Query Match      100.0%; Score 57; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 2.3e-05;
Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGGCAUGCGCUUGCGCAUGGAGGACCC 57
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DB 1 GGGTCCACCTCTCGCGGTCGCACTGGGCATCGCGCTTCGCATGCTGAAGGACCC 57

RESULT 9
LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"

ORIGIN
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Best Local Similarity 64.9%; Pred. No. 0.02;
Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGGCAUGCGCUUGCGCAUGGAGGACCC 57
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DB 1 GGGTCCACCTCTCGCGGTCGCACTGGGCATCGCGCTTCGCATGCTGAAGGACCC 57

RESULT 10
LOCUS AX012291 37 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 53 from Patent WO9955856.
ACCESSION AX012291
VERSION AX012291.1 GI:9998352
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 53 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
1..37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"

ORIGIN
Query Match      64.9%; Score 37; DB 6; Length 37;
Best Local Similarity 67.6%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGGCAUGCGGCGC 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 GGGTCCACCTCTCGCGGTCGCACTGGGCATGCGGCGC 37

RESULT 11
LOCUS HSA287B20/c 168545 bp DNA linear PRI 11-MAR-2001
DEFINITION Human DNA sequence from clone RP11-287B20 on chromosome 20 Contains
```

part of gene KIAA1272 for a protein similar to rat Tulip 2, ESTs, STSs and GSSs, complete sequence.

ACCESSION AL121896
VERSION AL121896.11 GI:12583641
KEYWORDS HTG; KIAA1272; Tulip.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168545)
Griffiths, C.
Direct Submission
Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

On Jan 27, 2001 this sequence version replaced gi:8218066.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
<http://www.sanger.ac.uk/projects/C.elegans/wormpep> This sequence
was generated from part of bacterial clone contigs of human
Chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr20>

Rp11-287B20 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone
Rp11-287B20 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone Rp11-287B20 is at 1 in this sequence.
The true left end of clone Rp5-1049G11 is at 168446 in this
sequence. The true right end of clone Rp11-470C13 is at 11612 in
this sequence. This sequence was finished as follows unless
otherwise noted: all regions were either double-stranded or
sequenced with an alternate chemistry or covered by high quality
data (i.e., phred quality >= 30); an attempt was made to resolve
all sequencing problems, such as compressions and repeats; all
regions were covered by at least one plasmid subclone or more than
one M13 subclone; and the assembly was confirmed by restriction
digest.

FEATURES

source
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="20"
/clone="Rp11-287B20"
/clone_lib="RPCI-11.1"
23..649

misc_feature

repeat_region
30..496
/note="match: GSS: Em:AQ542006"

repeat_region
30..496
/note="L1MB8 repeat: matches 5689. .6167 of consensus"

misc_feature
complement(358..678)
/note="match: STS: Em:G25753 Em:G27399"

repeat_region
2049..2584

repeat_region
5422..5607
/note="L2 repeat: matches 2101. .2670 of consensus"

repeat_region
5931..6206
/note="MER5B repeat: matches 1. .178 of consensus"

repeat_region
5931..6206
/note="AluJb repeat: matches 1. .275 of consensus"

misc_feature
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misc_feature
9279..9997
/note="match: STS: Em:G57973"

misc_feature

9283..9746
/note="match: GSS: Em:AQ345124"

misc_feature

complement(9548..10038)
/note="match: GSS: Em:AQ525450"

misc_feature

10005..10404
/note="match: GSS: Em:AQ727919"

gene

complement(11328..146133)
/note="match: GSS: Em:AQ409384"

CDS

/gene="BA287B20.1"
complement(join(<11328..11449,72130..72257,94418..94576,
102852..102807,104712..104835,110555..110626,
111814..112585,120218..120401,123707..123844,
124311..124199,125553..125663,130988..131096,
135046..135104,135957..136085,146005..146133))
/note="BA287B20.1"

/note="continued from dJ1049G11 (AL078634)"

match: CDNAs: Em:AK082211 Em:AB032400 Em:AF041106

Em:AF041107 Em:AL050050 Em:AB033098

match: ESTs: Em:T90823 Em:BB467241 Em:BE349987 Em:BE219600

Em:R05337 Em:T85728 Em:AW753998 Em:AW604552 Em:AW658646

Em:R05338

match: proteins: Tr:O55008 Tr:Q9Y408"

/codon_start=1

/evidence="not experimental"

/product="BA287B20.1.1 (KIAA1272 similar to rat tulip

proteins 1 and 2, isoform 1)"

/protein_id="CAC27349.1"

/db_xref="GI:12583643"

/db_xref="UniProt/TREMBL:Q9BQT6"

/translation="DILTIIRHCPFRFSLGFGFGFMSLVGDFITAAARVLSTDLTILTA
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SWYKIQMFETSLPRKMAEILVATVFLPSAEYSVETKKFVSLLLCLLDWCMAL
PVSLHPVSTAVLEQHSAPAPLDLYRVLHCCVCGSVTQOSHLYLTLDLSST
DYDPLPLANVASEPQVTHSSAELGNLLTVEEEKRRSLLELIPITARNMAHLVNHL
GHYPLSGFPAILHLSLVNSHDNAHVSELSFEVPRSNLQFVNDPSFLSYLQTPPT
EGPVGSGFVSLSDVRVIRVDISGKVLGYGLGCLAPNGRNPFLYSSWHRD
TFPGKDSQVEGDDVLDKLEINIGTSPCLPSQLNPNPSLTPCGMNTDQKEI
LEVLIRQNAODEVITQSHNFSAMKVTSGQSPVPRGPFYFCRLLDLGNWSDR
RKNPHLLKSKLLRELKLDLSROCRETHKTAIFYIAEGQEDKCSILNERSGOAYED
FVAGLGNVEDLTHCGFMGLQNRSGTQTAPYATSVTFVHFHVSINRPSDDSLT
FKRLHLDGVHIVMSEHSRYRGGIITAFGDVSIITPYPMKNHMFIAITKKPEVPFF
FGPLFGAIVSGKLLPSLVCACTINASRAVKCLIPLYQSFYBEERALYUEAITQNHREV
MTFEDFAAQVSPSPSYSLSGT"

11547..12050

/note="match: STS: Em:G55717"

match: GSS: Em:AQ312069"

12766..12980

/note="MER3 repeat: matches 4. .209 of consensus"

14926..15041

/note="FLAM A repeat: matches 20. .135 of consensus"

15330..15369

/note="MIR repeat: matches 106. .148 of consensus"

15335..15474

/note="MIR repeat: matches 70. .213 of consensus"

15634..15733

/note="MIR repeat: matches 81. .175 of consensus"

16054..16481

/note="match: GSS: Em:B47002"

16546..16696

/note="MLTIC repeat: matches 299. .466 of consensus"

16740..16951

/note="MLTIC repeat: matches 17. .237 of consensus"

17228..17518

/note="L1M4 repeat: matches 5031. .5329 of consensus"

17900..18040

/note="L1MD2 repeat: matches 5788. .5932 of consensus"

18042..18340

/note="AluJo repeat: matches 1. .298 of consensus"

19137..19367

/note="L2 repeat: matches 2515. .2748 of consensus"

20304..20689

/note="L1MB7 repeat: matches 5188. .5577 of consensus"

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 200542 bases at least Q40
Consensus quality: 209380 bases at least Q30
Consensus quality: 212903 bases at least Q20
Insert size: 250000; agarose-fp
Insert size: 215811; sum-of-contigs
Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 41 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1	1138:	contig of 1138 bp in length
1139	1238:	gap of 100 bp
1239	2528:	contig of 1290 bp in length
2529	2628:	gap of 100 bp
2629	3823:	contig of 1195 bp in length
3824	3923:	gap of 100 bp
3924	5052:	contig of 1129 bp in length
5053	5152:	gap of 100 bp
5153	6323:	contig of 1171 bp in length
6324	6423:	gap of 100 bp
6424	6930:	contig of 507 bp in length
6931	7030:	gap of 100 bp
7031	8598:	contig of 1568 bp in length
8599	8698:	gap of 100 bp
8699	10151:	contig of 1453 bp in length
10152	10251:	gap of 100 bp
10252	10680:	contig of 429 bp in length
10681	10780:	gap of 100 bp
10781	13715:	contig of 2935 bp in length
13716	13815:	gap of 100 bp
13816	16140:	contig of 2325 bp in length
16141	16240:	gap of 100 bp
16241	18860:	contig of 2620 bp in length
18861	18960:	gap of 100 bp
18961	21162:	contig of 2202 bp in length
21163	21262:	gap of 100 bp
21263	23366:	contig of 2104 bp in length
23367	23466:	gap of 100 bp
23467	23844:	contig of 2378 bp in length
25845	25944:	gap of 100 bp
25945	28531:	contig of 2587 bp in length
28532	28631:	gap of 100 bp
28632	32027:	contig of 3396 bp in length
32028	32127:	gap of 100 bp
32128	35156:	contig of 3029 bp in length
35157	35256:	gap of 100 bp
35257	38834:	contig of 3578 bp in length
38835	38934:	gap of 100 bp
38935	42147:	contig of 3213 bp in length
42148	42247:	gap of 100 bp
42248	45992:	contig of 3745 bp in length
45993	46092:	gap of 100 bp
46093	49628:	contig of 3536 bp in length
49629	49728:	gap of 100 bp
49729	53348:	contig of 3620 bp in length
53349	53448:	gap of 100 bp
53449	57318:	contig of 3870 bp in length
57319	57418:	gap of 100 bp
57419	61725:	contig of 4307 bp in length
61726	61825:	gap of 100 bp
61826	66467:	contig of 4642 bp in length
66468	66567:	gap of 100 bp
66568	71527:	contig of 4960 bp in length
71528	71627:	gap of 100 bp
71628	76418:	contig of 4791 bp in length

```

misc_feature      35257..38834

Query Match      54.7%; Score 31.2; DB 2; Length 219811;
Best Local Similarity 47.7%; Pred.No.5.5e+02;
Matches 21; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY      8  CCUCCUGCGGUNNNNUGCGGCAUGCGGCGUCCGCAUGGCUAAG 51
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      61537  CCTCCTCTGTGTGGCTATGGCATGTGCCTCCCTGCCTATG 61580

RESULT 14
AL929212/c
LOCUS           AL929212      255261 bp      DNA      linear      ROD 01-APR-2003
DEFINITION      Mouse DNA sequence from clone RP23-65G6 on chromosome 2, complete
                 sequence.
ACCESSION       AL929212
VERSION         AL929212.8  GI:29466488
KEYWORDS        HTG.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE       1  (bases 1 to 255261)
AUTHORS         Tracey,A.
TITLE           Direct Submission
JOURNAL         Submitted (01-APR-2003) Wellcome Trust Sanger Institute, Hinxton,
                Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT         On Apr 1, 2003 this sequence version replaced gi:28445802.
                Sequence from the Mouse Genome Sequencing Consortium whole genome
                shotgun may have been used to confirm this sequence. Sequence data
                from the whole genome shotgun alone has only been used where it has
                a phred quality of at least 30.
                ----- Genome Center
                Center: Wellcome Trust Sanger Institute
                Center code: SC
                Web site: http://www.sanger.ac.uk
                Contact: humquerry@sanger.ac.uk
                -----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
EMBL, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPF; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep/
from the RPCI-23 Mouse BAC library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6.
          Location/Qualifiers
            1..255261
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /db_xref="taxon:10090"
               /chromosome="2"
               /clone="RP23-65G6"
               /clone_lib="RPCI-23"
FEATURES
source
ORIGIN

```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:06:47 ; Search time 2476.25 Seconds
(without alignments)
876.189 Million cell updates/sec

Title: US-09-699-667E-61
Perfect score: 57
Sequence: 1 ggguccaccuccucggun.....uucgaugcuaggagacc 57

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	33	57.9	857	7 CF552723	CF552723 AGENCOURT
C 2	32.8	57.5	1182	4 BI457296	BI457296 603185617
C 3	32.2	56.5	622	9 CC526419	CC526419 CH240.401
C 4	31.8	55.8	726	2 BF686394	BF686394 602143774
C 5	31.8	55.8	807	2 BE902113	BE902113 601674890
C 6	31.4	55.1	869	6 CB991305	CB991305 AGENCOURT
C 7	31	54.4	382	2 AW681122	AW681122 WS1_8_E02
C 8	31	54.4	405	2 AW681043	AW681043 WS1_8_E02
C 9	31	54.4	448	2 AW283452	AW283452 LG1_272_E
C 10	31	54.4	537	9 CL629016	CL629016 OR_Bsa002
C 11	31	54.4	694	9 CL713844	CL713844 OR_Bsa003
C 12	31	54.4	723	9 CL173974	CL173974 104_377_1
C 13	31	54.4	726	9 CL173973	CL173973 104_377_1
C 14	31	54.4	822	7 CN127442	CN127442 RHOH1_23
C 15	31	54.4	1057	4 BM553956	BM553956 AGENCOURT
C 16	30.8	54.0	808	2 BE901025	BE901025 601674156
C 17	30.6	53.7	538	2 BE682984	BE682984 181389_MA
C 18	30.6	53.7	777	4 BF796052	BF796052 602259070
C 19	30.6	53.7	808	4 BM006402	BM006402 603615114
C 20	30.6	53.7	823	9 CC593873	CC593873 CH240.395
C 21	30.4	53.3	658	7 CR363279	CR363279 CR363279
C 22	30.4	53.3	971	2 BE794244	BE794244 601591516
C 23	30.4	53.3	1107	2 BE562270	BE562270 601344732
C 24	30.2	53.0	339	9 CL316408	CL316408 ZMMB8c037

C 25	30.2	53.0	495	4 BJ004361	BJ004361 BJ004361
C 26	30.2	53.0	513	2 BE386169	BE386169 601274411
C 27	30.2	53.0	837	4 BJ728719	BJ728719 BJ728719
C 28	30	52.6	123	1 AU077016	AU077016 AU077016
C 29	30	52.6	210	7 CR767128	CR767128 DKFZp469L
C 30	30	52.6	222	7 CF122359	CF122359 UI-HF-CB0
C 31	30	52.6	257	4 BM798589	BM798589 K-EST0082
C 32	30	52.6	294	1 AI651473	AI651473 W060609.X
C 33	30	52.6	300	1 AU099987	AU099987 AU099987
C 34	30	52.6	328	1 AI825463	AI825463 W073C03.X
C 35	30	52.6	349	6 CB126416	CB126416 K-EST0175
C 36	30	52.6	364	7 CN257892	CN257892 170006001
C 37	30	52.6	370	1 AL701336	AL701336 DKFZp886L
C 38	30	52.6	379	6 C19347	C19347 C19347 Rice
C 39	30	52.6	380	6 CB144469	CB144469 K-EST0198
C 40	30	52.6	390	6 CD609316	CD609316 56067704H
C 41	30	52.6	391	7 CN257890	CN257890 170006002
C 42	30	52.6	404	1 AU067971	AU067971 AU067971
C 43	30	52.6	428	6 C23613	C23613 C23613 Rice
C 44	30	52.6	428	7 CF144607	CF144607 UI-HF-CB0
C 45	30	52.6	453	4 BM836423	BM836423 K-EST0112

ALIGNMENTS

RESULT 1
CF552723/c 857 bp mRNA linear EST 22-SEP-2003
LOCUS AGENCOURT15595333 NIH_MGC_183 Homo sapiens cDNA clone
DEFINITION IMAGE:30529107 5', mRNA sequence.
ACCESSION CF552723
VERSION CF552723.1 GI:34889557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 857)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM616 row: c column: 04
High quality sequence stop: 680.

FEATURES

Location/Qualifiers
1..857
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30529107"
/lab_host="DH10B-Tona (T1 and T5 phage resistant)"
/clone_lib="NIH MGC 183"
/note="Organ: Pooled muscle (cardiac and skeletal);
vector: pCMV-SF016.1; Site_1: EcoRV (destroyed); Site_2:
NotI; Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.7. Library was constructed by Invitrogen."

ORIGIN

Query Match 57.9%; Score 33; DB 7; Length 857;
Best Local Similarity 50.9%; Pred. No. 1.7e+02;


```

ORIGIN
Query Match      55.1%; Score 31.4; DB 6; Length 869;
Best Local Similarity 51.0%; Pred. No. 5.6e+02;
Matches 25; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY    1  GGGUCCACCUCCUCGCGGUNNNNNNGGCAGUCGCGCTTCGAUGGCUA 49
      |||||:||||:||||:||||:||||:||||:||||:||||:

```


/db_xref="taxon:4558"
 /clone_lib="Light Grown 1 (LGI)"
 /notes="Organ: 10- to 14-day-old light-grown (greenhouse)
 seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
 EcoRI; The library was made from poly-A RNA in the cloning
 vector lambda ZAP II. Clones to be sequenced were
 prepared by mass excision."

ORIGIN

Query Match 54.4%; Score 31; DB 2; Length 448;
 Best Local Similarity 49.1%; Pred. No. 6.9e+02;
 Matches 27; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 GGUCCACUCCUCCGGGUNNNNUGGCGAUGCGUCCGUAAGGGAC 55
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
 Db 75 GGTTCAGCTCTCCACGACCTGGCTGATCGCATAGCATGCCAAGGGAC 129

RESULT 10

CL629016 537 bp DNA linear GSS 01-JUL-2004
 LOCUS OR_BBa0028L22.f OR_BBa Oryza rufipogon genomic clone OR_BBa0028L22
 DEFINITION 5'- genomic survey sequence.

ACCESSION CL629016 GI:49134446
 VERSION GSS.
 KEYWORDS
 SOURCE ORGANISM

Oryza rufipogon
 Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 537)
 AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

TITLE OMAP Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: TAA TAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 161 Std Error: 0.00
 Plate: 0028 row: L column: 22
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..537
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BBa0028L22"
 /tissue_type="young leaves"
 /lab_host="DH10B-T1 phage resistant"
 /clone_lib="OR_BBa"
 /notes="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 54.4%; Score 31; DB 9; Length 537;
 Best Local Similarity 50.9%; Pred. No. 7.1e+02;
 Matches 28; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 GGUCCACUCCUCCGGGUNNNNUGGCGAUGCGUCCGUAAGGGAC 56
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
 Db 377 GGGCCAGCATCTCGCATCGCACTTGGCTTGGCGAGTCATGCTCAATGGCC 431

RESULT 11

CL713844

LOCUS CL713844 694 bp DNA linear GSS 26-JUL-2004
 DEFINITION OR_BBa0038P20.r OR_BBa Oryza rufipogon genomic clone OR_BBa0038P20
 3', genomic survey sequence.

ACCESSION CL713844
 VERSION GSS.
 KEYWORDS
 SOURCE ORGANISM

Oryza rufipogon
 Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 694)
 AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

TITLE OMAP Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 161 Std Error: 0.00
 Plate: 0038 row: F column: 20
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.

Location/Qualifiers
 1..694
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BBa0038P20"
 /tissue_type="young leaves"
 /lab_host="DH10B-T1 phage resistant"
 /clone_lib="OR_BBa"
 /notes="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

Query Match 54.4%; Score 31; DB 9; Length 694;
 Best Local Similarity 50.9%; Pred. No. 7.3e+02;
 Matches 28; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 GGUCCACUCCUCCGGGUNNNNUGGCGAUGCGUCCGUAAGGGAC 56
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
 Db 376 GGGCCAGCATCTCGCATCGCACTTGGCTTGGCGAGTCATGCTCAATGGCC 430

ORIGIN

Query Match 54.4%; Score 31; DB 9; Length 694;
 Best Local Similarity 50.9%; Pred. No. 7.3e+02;
 Matches 28; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

RESULT 12

CL713974/c

LOCUS CL713974 723 bp DNA linear GSS 06-JAN-2004
 DEFINITION 104_377_10891241_148_31792_377 Sorghum methylation-filtered library
 (LibID: 104) Sorghum bicolor genomic clone 10891241, genomic survey
 sequence.

ACCESSION CL713974
 VERSION CL713974.1 GI:40686420
 KEYWORDS GSS.
 SOURCE ORGANISM

Sorghum bicolor (sorghum)
 Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 723)
 AUTHORS Budiman,M.A., Flick,E., Jones,J., Rao,K., Luo,M., Jetty,R.W.,
 Robbins,D., Rohlfing,T., Bradford,K., Fries,J., McMenamy,J.,
 Trani,L., Isak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.

TITLE Genethresher methylation filtered genomic sequences from Sorghum
 bicolor

JOURNAL Unpublished (2004)

COMMENT Contact: Bedell JA

Search completed: March 15, 2005, 15:20:12
Job time : 2484.25 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:52:23 ; Search time 372.25 Seconds
(without alignments)
910.856 Million cell updates/sec

Title: US-09-699-667E-62
Perfect score: 57
Sequence: 1 ggguccacucccgcggn.....cgggcaugcuaggagacc 57

Scoring table: IDENTITY NUCDX
Gapop 10_0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 5307542

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/FCIUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29.4	51.6	52	17	US-10-346-880-40
2	29.4	51.6	52	17	US-10-346-880-80
3	29.4	51.6	52	17	US-10-150-407-40
4	29.4	51.6	52	17	US-10-150-407-80
5	29	50.9	56	17	US-09-507-362-39
6	29	50.9	56	17	US-10-391-441-39
C 7	24	42.1	51	18	US-10-628-109-118
C 8	24	42.1	51	18	US-10-628-109-106
C 9	24	42.1	55	18	US-10-628-109-107
C 10	24	42.1	55	18	US-10-628-109-108
C 11	23.8	41.8	60	19	US-10-612-468A-86
					Sequence 40, Appl
					Sequence 80, Appl
					Sequence 80, Appl
					Sequence 39, Appl
					Sequence 118, Appl
					Sequence 106, Appl
					Sequence 107, Appl
					Sequence 108, Appl
					Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-10-346-880-40
; Sequence 40, Application US/10346880
; Publication No. US2003023035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0

Sequence 105, App
Sequence 15052, A
Sequence 3088, Ap
Sequence 7, Appl
Sequence 119, App
Sequence 121, App
Sequence 2265, Ap
Sequence 111, App
Sequence 13039, A
Sequence 18325, A
Sequence 19116, A
Sequence 98, Appl
Sequence 381, App
Sequence 382, App
Sequence 382, App
Sequence 381, App
Sequence 382, App
Sequence 5, Appl
Sequence 1234, Ap
Sequence 9, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 113, App
Sequence 606, App
Sequence 109, App
Sequence 7514, Ap
Sequence 1308, Ap
Sequence 6, Appl
Sequence 5639, Ap
Sequence 177, App
Sequence 704, App
Sequence 600, App
Sequence 332, App

```
; SEQ ID NO 40
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match
Best Local Similarity 51.6%; Score 29.4; DB 17; Length 52;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCAUGC 34
Db 1 TCACCTCTCGCGTCCGACCTGGGCATCC 31

RESULT 2
US-10-346-880-80
; Sequence 80, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

Query Match
Best Local Similarity 51.6%; Score 29.4; DB 17; Length 52;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCAUGC 34
Db 1 TCACCTCTCGCGTCCGACCTGGGCATCC 31

RESULT 3
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-150-407-40

Query Match 51.6%; Score 29.4; DB 17; Length 52;
Best Local Similarity 58.1%; Pred. No. 66;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNNUGGCAUGC 34
Db 1 TCACCTCTCGCGTCCGACCTGGGCATCC 31

RESULT 4
US-10-150-407-80
; Sequence 80, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-150-407-80

Query Match 51.6%; Score 29.4; DB 17; Length 52;
Best Local Similarity 58.1%; Pred. No. 66;
Matches 18; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCAUC 34
Db 1 TCCACCTCTCGCGTCCGACCTGGCATCC 31

RESULT 5
US-09-507-362-39
; Sequence 39, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match 50.9%; Score 29; DB 17; Length 56;
Best Local Similarity 58.6%; Pred. No. 91;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCAU 32
Db 27 TCCACCTCTCGCGTCCGACCTGGCAT 55

RESULT 6
US-10-391-441-39
; Sequence 39, Application US/10391441
; Publication No. US20030232058A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,441
; FILING DATE: 17-Mar-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match 50.9%; Score 29; DB 17; Length 56;
Best Local Similarity 58.6%; Pred. No. 91;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNUGGCAU 32
Db 27 TCCACCTCTCGCGTCCGACCTGGCAT 55
```

RESULT 7
US-10-628-109-118/c
; Sequence 118, Application US/10628109
; Publication No. US20040101886A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: McWhirter, John
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
; FILE REFERENCE: 1087-35 DIV
; CURRENT APPLICATION NUMBER: US/10/628,109
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/254,669
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/323,400
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 10/014,012
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 51
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nesting oligonucleotide
US-10-628-109-118

Query Match 42.1%; Score 24; DB 18; Length 51;
Best Local Similarity 47.5%; Pred. No. 4.2e+03;
Matches 19; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGUCCACCUCCUGCGGUNNNNNNUGGCAUGCCUUCGGG 41
DB 40 GCTGCACCTCTCTCGAGGGCCGCTTTCGGGGCCCTCGAG 1

RESULT 8
US-10-628-109-106/c
; Sequence 106, Application US/10628109
; Publication No. US20040101886A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: McWhirter, John
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
; FILE REFERENCE: 1087-35 DIV
; CURRENT APPLICATION NUMBER: US/10/628,109
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/254,669
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/323,400
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 10/014,012
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
; LENGTH: 55
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nesting oligonucleotide
US-10-628-109-106

Query Match 42.1%; Score 24; DB 18; Length 55;

Best Local Similarity 47.5%; Pred. No. 4.3e+03;
Matches 19; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGUCCACCUCCUGCGGUNNNNNNUGGCAUGCCUUCGGG 41
DB 40 GCTGCACCTCTCTCGAGGGCCGCTTTCGGGGCCCTCGAG 1

RESULT 9
US-10-628-109-107/c
; Sequence 107, Application US/10628109
; Publication No. US20040101886A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: McWhirter, John
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
; FILE REFERENCE: 1087-35 DIV
; CURRENT APPLICATION NUMBER: US/10/628,109
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/254,669
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/323,400
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 10/014,012
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 55
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nesting oligonucleotide
US-10-628-109-107

Query Match 42.1%; Score 24; DB 18; Length 55;
Best Local Similarity 47.5%; Pred. No. 4.3e+03;
Matches 19; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGUCCACCUCCUGCGGUNNNNNNUGGCAUGCCUUCGGG 41
DB 40 GCTGCACCTCTCTCGAGGGCCGCTTTCGGGGCCCTCGAG 1

RESULT 10
US-10-628-109-108/c
; Sequence 108, Application US/10628109
; Publication No. US20040101886A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: McWhirter, John
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
; FILE REFERENCE: 1087-35 DIV
; CURRENT APPLICATION NUMBER: US/10/628,109
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/254,669
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/323,400
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 10/014,012
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 108
; LENGTH: 55

; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nesting oligonucleotide
US-10-628-109-108

Query Match 42.1%; Score 24; DB 18; Length 55;
Best Local Similarity 47.5%; Pred. No. 4.3e+03;
Matches 19; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGUCCACUCCUGCGGUNNNNNNUGGCAUGCCUUCGGG 41
DB 40 GCTGCACCTCTCGAGGGCCGCTTTTCGGGGCCCTCGAG 1

RESULT 11

US-10-612-468A-86
; Sequence 86, Application US/10612468A
; Publication No. US20050010030A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jingwu Z.
; APPLICANT: Ho, Walter Kowk Keung
; APPLICANT: Zhang, Donging
; APPLICANT: Sun, Wei
; TITLE OF INVENTION: T Cell Receptor CDR3 Sequence and Methods for Detecting
; TITLE OF INVENTION: and Treating Rheumatoid Arthritis
; FILE REFERENCE: 057186.000003
; CURRENT APPLICATION NUMBER: US/10/612,468A
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 86
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: CDR3 nucleic acid sequence of BV16 cloneotype derived
; OTHER INFORMATION: from ST specimen of RA patients
US-10-612-468A-86

Query Match 41.8%; Score 23.8; DB 19; Length 60;
Best Local Similarity 46.5%; Pred. No. 5e+03;
Matches 20; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 5 CCACUCCUGCGGUNNNNNNUGGCAUGCCUUCGGGCAUGGC 47
DB 18 CCTTCTGGGACAGATATCTATGAGCAGTTCCTTCGGGGCCAGGC 60

RESULT 12

US-10-628-109-105/c
; Sequence 105, Application US/10628109
; Publication No. US2004010186A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: McWhirter, John
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
; TITLE OF INVENTION: AMPLIFICATION
; FILE REFERENCE: 1087-35 DIV
; CURRENT APPLICATION NUMBER: US/10/628,109
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/254,669
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/323,400
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 10/014,012
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 105

; LENGTH: 55
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nesting oligonucleotide
US-10-628-109-105

Query Match 41.4%; Score 23.6; DB 18; Length 55;
Best Local Similarity 45.0%; Pred. No. 5.8e+03;
Matches 18; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGUCCACUCCUGCGGUNNNNNNUGGCAUGCCUUCGGG 41
DB 40 GCTGCACCTCTCGAGGGCCGCTTTTCGGGGCCCTCGAG 1

RESULT 13

US-09-908-975-15052/c
; Sequence 15052, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15052
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-15052

Query Match 41.4%; Score 23.6; DB 10; Length 60;
Best Local Similarity 41.3%; Pred. No. 5.8e+03;
Matches 19; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 2 GGUCCACUCCUGCGGUNNNNNNUGGCAUGCCUUCGGGCAUGGC 47
DB 58 GCTGCACCATCTCGCGGCTGCTACTTGACGATCTCTGGATGATGC 13

RESULT 14

US-10-349-143-3088/c
; Sequence 3088, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796

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Query Match      39.3%; Score 22.4; DB 10; Length 39;
Best Local Similarity 58.3%; Pred. NO. 1.4e+04;
Matches 14; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy      8  CCUCCUGCGGUNNNNNNUGGGCA 31
      ||:||||| ::::|||||
Db     16  CCTCCTCGCGCGCGGATGGGCA 39

Search completed: March 15, 2005, 21:09:21
Job time : 373.25 secs

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; SEQ ID NO 3088
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-22706-367 : polymorphic base T or C
US-10-349-143-3088

Query Match 40.7%; Score 23.2; DB 17; Length 47;
Best Local Similarity 38.6%; Pred. No. 7.8e+03;
Matches 17; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

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```

RESULT 15
US-09-991-262-7
; Sequence 7, Application US/09991262
; Publication No. US20030041349A1
; GENERAL INFORMATION:
; APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
; TITLE OF INVENTION: Insect Viruses and Their Uses in
; Protecting Plants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/991,262
; FILING DATE: 20-No. US20030041349A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,238
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: US 08/485,355
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/440,522
; FILING DATE: 12-MAY-1995
; APPLICATION NUMBER: US 08/089,372
; FILING DATE: 08-JUL-1993
; APPLICATION NUMBER: AU PL4081/92
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard P.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58631-3/RFT/DSS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-991-262-7

```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 01:00:51 ; Search time 315.5 Seconds
(without alignments)
1069.494 Million cell updates/sec

Title: US-09-699-667E-61

Perfect score: 57

Sequence: 1 ggguccaccuccgcggun.....uucgauggcuaagggaccc 57

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	57	3	Aaz57636 Trans-act
2	57	100.0	57	3	Aaz57637 Trans-act
3	47.4	83.2	57	3	Aaz57638 Trans-act
4	35.4	62.1	37	3	Aaz57639 Nucleotid
5	31.8	55.8	61	2	AaQ46667 Substrate
6	30.6	53.7	138627	12	AdQ97183 Human can
7	30.4	53.3	48	13	Adr47040 Dengue vi
8	30.4	53.3	48	13	Adt48965 PCR prime
9	30.4	53.3	51	2	AaQ86173 Primer HD
10	30.4	53.3	52	2	AaQ86204 Sindbis/H
11	30.4	53.3	52	2	Aat31151 HDV rever
12	30.4	53.3	52	2	Aat30817 HDV riboz
13	30.4	53.3	52	2	Aav42394 Nested PC
14	30.4	53.3	52	2	Aav42426 Forward P
15	30.4	53.3	52	2	Aav60154 Nested PC
16	30.4	53.3	52	2	Aav60185 Reversee P
17	30.4	53.3	52	2	Aav70746 Reversee P
18	30.4	53.3	52	2	Aav70714 Nested pr
19	30.4	53.3	52	3	Aaz292930 Hepatitis
20	30.4	53.3	52	3	Aaz292970 Hepatitis

21	30.4	53.3	52	3	Aaz292843	Aaz292843 Hepatitis
22	30.4	53.3	52	3	Aaz292803	Aaz292803 Hepatitis
23	30.4	53.3	52	6	Aal38850	Aal38850 Alphaviru
24	30.4	53.3	52	6	Aal38810	Aal38810 Alphaviru
25	30.4	53.3	52	6	Abk46276	Abk46276 HDV antiq
26	30.4	53.3	52	6	Abk46316	Abk46316 Hepatitis
27	30.4	53.3	52	12	Adi30383	Adi30383 Hepatitis
28	30.4	53.3	52	12	Adi30423	Adi30423 Hepatitis
29	30.4	53.3	52	12	Ado13982	Ado13982 Eukaryoti
30	30.4	53.3	52	12	Ado13942	Ado13942 Eukaryoti
31	30.4	53.3	57	12	Adh10551	Adh10551 Hepatitis
32	30.4	53.3	80	2	AaQ53138	AaQ53138 Substrate
33	30.4	53.3	80	2	AaQ53140	AaQ53140 Substrate
34	30.4	53.3	83	5	Aaf28121	Aaf28121 HDV riboz
35	30.4	53.3	84	13	Adr47033	Adr47033 Dengue vi
36	30.4	53.3	85	2	AaQ46665	AaQ46665 Self-clea
37	30.4	53.3	86	2	AAO46663	AAO46663 Self-clea
38	30.4	53.3	90	2	Aax76586	Aax76586 Hepatitis
39	30.4	53.3	90	5	Aaf84035	Aaf84035 EPO gene
40	30.4	53.3	90	5	AAf84036	AAf84036 EPO gene
41	30.4	53.3	91	8	ABZ82120	ABZ82120 Hepatitis
42	30.4	53.3	94	12	ADP96249	ADP96249 HEP rabie
43	30.4	53.3	99	8	ABZ82121	ABZ82121 Hepatitis
44	30.4	53.3	567	1	AAH82174	AAH82174 Clone del
45	30.4	53.3	1369	12	ADH10576	ADH10576 Nucleotid

ALIGNMENTS

RESULT 1
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
XX
AC AAZ57636;
XX
DT 05-APR-2000 (first entry)
DE Trans-acting antigenomic delta ribozyme, deltaRzPl.1 nucleotide sequence.
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX inherited disease; deltaRzPl.1; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound moiety= "SP1.1 substrate (AAZ57641) bases 5-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX
XX WO9955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX (UYSH) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
DR


```

PA (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
XX diagnostic and therapeutic applications.
XX
XX Example 1; Fig 2; 52pp; English.
XX
XX This is the nucleotide sequence of a trans-acting antigenomic delta
XX ribozyme of the invention. This ribozyme cleaves substrate Sp1.1 (see
XX AA257641). The invention relates to a nucleic acid enzyme (e.g.
XX deltaRzP1.1) that is constructed to have a substrate binding portion with
XX the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
XX sequence 5'-H*GNHNN-3'. The binding portion of the enzyme (ribozyme)
XX base pairs to 6 nucleotides 3' to the cleavage site of the substrate
XX (cleavage site is represented by *). At least one nucleotide is present
XX 5' to the cleavage site of the substrate sequence. The enzyme of the
XX invention is used to cleave a substrate nucleotide sequence at a specific
XX cleavage site by mixing the substrate with the enzyme. The enzyme is used
XX to cleave viral RNA or RNA causing for example an inherited disease. The
XX enzymes also have other therapeutic, biotechnological and diagnostic
XX applications. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match 83.2%; Score 47.4; DB 3; Length 57;
Best Local Similarity 78.9%; Pred. NO. 0.00032;
Matches 45; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGUCCACCUCUCGCGUNNNNUGGCGAUGGCGUUCGCAUGGCUAAGGGACCC 57
Db 1 GGGUCCACCUCUCGCGUCCGCCGCGAUGGCGUUCGCGGCAUGGCGUUCGCGACCC 57

RESULT 4
AAZ57639
ID AAZ57639 standard; RNA; 37 BP.
XX
XX AAZ57639;
XX
XX 05-APR-2000 (first entry)
XX
XX Nucleotide sequence of bimolecular ribozyme RZA fragment.
XX
XX Bimolecular ribozyme; viral RNA cleavage; RZA fragment;
XX inherited disease; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /tag= a
FT /bound_moiety= "RzB fragment of bimolecular ribozyme"
FT /note= "Forms double-stranded region with bases 20-16 of
FT sequence AAZ57640"
FT stem_loop 7..19
FT /tag= b
FT /tag= 20..25
FT /tag= c
FT /bound_moiety= "Ribozyme substrate P1.1"
FT /note= "Forms double-stranded region with bases 11-6 of
FT sequence AAZ57641"
FT misc_binding 30..37
FT /tag= d
FT /bound_moiety= "RzB fragment of bimolecular ribozyme"
FT /note= "Forms double-stranded region with bases 8-1 of
FT sequence AAZ57640"
XX
XX WO9955856-A2.
XX
XX

```

Pd		04-NOV-1999.
Xx		
Ff		29-APR-1999; 99WO-CA000391.
Xx		
Pp		29-APR-1998; 98CA-02230203.
Xx		(UYSH) UNIV SHERBROOKE.
Fa		
Xx		Perreault J, Ananvoranich S, Lafontaine D;
Pt		WPI; 2000-096791/08.
Dn		
Xx		New construction of nucleic acid enzyme useful for biotechnological,
Ft		diagnostic and therapeutic applications.
Pt		
Xx		Example 5; Fig 4; 52pp; English.
Pg		This is the nucleotide sequence bimolecular ribozyme RZA fragment. This
Cc		ribozyme cleaves substrate SP1.1 (see AAZ57641). The invention relates to
Cc		a nucleic acid enzyme (e.g. deltaRpI.1) that is constructed to have a
Cc		substrate binding portion with the following sequence 3'-UNNXXN-5'. The
Cc		substrate of the enzyme has the sequence 5'-H'*GNHHNN-3'. The binding
Cc		portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
Cc		cleavage site of the substrate (cleavage site is represented by *). At
Cc		least one nucleotide is present 5' to the cleavage site of the substrate
Cc		sequence. The enzyme of the invention is used to cleave a substrate
Cc		nucleotide sequence at a specific cleavage site by mixing the substrate
Cc		with the enzyme. The enzyme is used to cleave viral RNA or DNA causing
Cc		for example an inherited disease. The enzymes also have other
Cc		therapeutic, biotechnological and diagnostic applications
Xx		
Sq		Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;
	Query Match	62.1%; Score 35.4; DB 3; Length 37;
	Best Local Similarity	81.1%; Pred.No.1.8;
	Matches 30; Conservative	6; Mismatches 1; Indels 0; Gaps 0;
Oy	1	GCGUCCACCUCCUGGCGGUNNNNNNGGGGAUCGCCGC 37
Db	1	GCGUCCACCUCCUGGCGGUCCGACCUGGGCAUGC GCC 37
	RESULT 5	
AQ	AAQA46667	AAQA46667 standard; RNA; 61 BP.
Xx	AAQA46667;	
Dt	25-MAR-2003 (revised)	
Dt	13-JAN-1994 (first entry)	
Xx		
De	Substrate-cleaving sequence ADC3.	
Xw	Substrate; self-cleaving sequence; HDV; hepatitis delta virus; enzyme;	
Kw	duplic; ss.	
Xx		
Os	Synthetic.	
Fh	Key	Location/Qualifiers
Ft	stem_loop	7..55
Ft		/tag= a
Ft	misc_structure	7..10
Ft		/tag= b
Ft		/label= stem_II
Ft		/note= "forms duplex with region 52..55"
Ft	stem_loop	11..23
Ft		/tag= d
Ft	misc_structure	11..13
Ft		/tag= e
Ft		/label= stem_III
Ft		/note= "forms duplex with region 21..23"
Ft	misc_feature	21..23
Ft		/tag= f
Ft		

XX
PN
XX

```
FT /label= stem_III
FT /note= "forms duplex with region 11..13"
FT misc_structure 24..30
FT /tag= g
FT /note= "RNA substrate binding region"
FT misc_structure 33..37
FT /tag= i
FT /label= stem_IV
FT /note= "forms duplex with region 42..45"
FT stem_loop 34..45
FT /tag= h
FT misc_feature 42..45
FT /tag= j
FT /label= stem_IV
FT /note= "forms duplex with region 33..37"
FT misc_feature 52..55
FT /tag= c
FT /label= stem_II
FT /note= "forms duplex with region 7..10"
XX WO9314218-A1.
XX
XX 22-JUL-1993.
XX
XX 12-JAN-1993; 93WO-US000292.
XX
XX 13-JAN-1992; 92US-00821155.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Been MD, Rosenstein SP, Perrota AT;
XX
XX WPI; 1993-243233/30.
XX
XX Nucleic acid molecule having RNA substrate-cleaving enzymatic activity -
XX useful for cleaving specific target molecules in-vitro.
XX
XX Disclosure; Fig 8; 55pp; English.
XX
XX The self-cleaving sequences from genomic and antigenomic HDV can be used
XX to develop enzymatic RNA mols. with similar properties. ADC3 is a smaller
XX version of ADC1 (AAQ53138), wherein stem IV is shortened. Such a smaller
XX enzymatic RNA has simplified synthesis and the potential for higher
XX specific activity due to a higher probability that a small RNA will fold
XX into an enzymatically active structure. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Sequence 61 BP; 10 A; 20 C; 19 G; 0 T; 12 U; 0 Other;
XX
XX Query Match 55.8%; Score 31.8; DB 2; Length 61;
XX Best Local Similarity 77.4%; Pred. No. 29;
XX Matches 41; Conservative 6; Mismatches 2; Indels 4; Gaps 1;
XX
XX 4 UCCACCUCUCCGCGGUNNNNUGGCAUGCGGCUUGCAUGGUAAGGACC 56
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 8 UCCACCUCUCCGCGGUGCGACCUUGGCAU---CUUGCGAUGGCUAAGGAGC 56
XX
XX
XX RESULT 6
XX ADQ97183/c
XX ID ADQ97183 standard; DNA; 138627 BP.
XX
XX AC ADQ97183;
XX
XX 07-OCT-2004 (first entry)
XX
XX Human cancer associated sequence HD08-011, SEQ ID 159.
XX
XX Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.
XX
XX Homo sapiens.
XX
XX WO2004060304-A2.
XX
XX PN
```

```
XX 22-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US041389.
XX
XX 27-DEC-2002; 2002US-00330773.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Malandro MS;
XX
XX WPI; 2004-543781/52.
XX
XX New isolated cancer associated nucleic acids comprising at least 10
XX contiguous nucleotides, useful for diagnosing, preventing and/or treating
XX cancers such as leukemia and lymphoma.
XX
XX Claim 1; SEQ ID NO 159; 199pp; English.
XX
XX The present invention relates to cancer associated sequences (ADQ97025-
XX ADQ98004). The sequences are useful for the diagnosis, prevention and/or
XX treatment of cancer, such as leukemia and lymphoma. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 138627 BP; 33083 A; 34745 C; 35023 G; 35281 T; 0 U; 495 Other;
XX
XX Query Match 53.7%; Score 30.6; DB 12; Length 138627;
XX Best Local Similarity 49.1%; Pred. No. 4.5e+02;
XX Matches 26; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
XX
XX 5 CCACCUCCUCCGCGGUNNNNUGGCAUGCGGCUUGCAUGGUAAGGAGCCC 57
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 79757 CCACCTCTGGCTGATGACITGGGCAAGGGGCTTCCCATCATCATGTTCCC 79705
XX
XX
XX RESULT 7
XX AD47040
XX ID AD47040 standard; DNA; 48 BP.
XX
XX AC AD47040;
XX
XX 18-NOV-2004 (first entry)
XX
XX Dengue virus vaccine oligonucleotide #15.
XX
XX ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
XX prem protein; C protein; NS1 protein signal; vaccine; cervical cancer;
XX viral disease; antigen; dendritic cell; immune response;
XX human papillomavirus.
XX
XX Unidentified.
XX
XX WO2004072274-A1.
XX
XX 26-AUG-2004.
XX
XX 30-JAN-2004; 2004WO-CN0000088.
XX
XX 30-JAN-2003; 2003CN-00115272.
XX
XX 30-JAN-2003; 2003CN-00115273.
XX
XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
XX
XX (TENG-) TENGGEN BIOMEDICAL CO.
XX
XX (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX
XX Pang X;
XX
XX WPI; 2004-625870/50.
XX
XX Virus-like particle vaccines containing dengue virus recombinant replicon
XX as core for carrier, applicable in preventives or/and remedies for tumors
XX
```

PT like cervical cancer and viral diseases.
 PS Example 4; SEQ ID NO 37; 38pp; Chinese.
 CC A dengue virus recombinant replicon has a deletion of the complete coding
 CC sequence for preM protein of dengue virus and also includes elements of
 CC e.g. the non-coding region in the whole of the 5'-end, the coding region
 CC of the front 20 amino acids in the C protein, and the coding region of
 CC NS1 protein signal; coding regions of all non-structural proteins. The
 CC obtained vaccines are useful in producing preventives or/and remedies for
 CC cancer like cervical cancer and viral diseases. Such vaccines can
 CC efficiently express antigen in infected cells, which is because dengue
 CC virus can infect dendritic cells, and can effectively present antigen to
 CC provide immunity effect. Different types of dengue virus can be used to
 CC repeatedly produce efficient immune response thereby strengthening the
 CC body's immune system against the pathogen that contains such antigen.
 CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
 CC expressing system using of the full-length dengue virus cDNA clone
 CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
 CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
 CC lines. This sequence corresponds to an oligonucleotide used in the
 CC recombinant replicon of the invention.
 XX
 SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
 Query Match 53.3%; Score 30.4; DB 13; Length 48;
 Best Local Similarity 59.4%; Pred. No. 75;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGUNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 17 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 48
 RESULT 9
 AAQ86173
 ID AAQ86173 standard; DNA; 51 BP.
 XX
 AC AAQ86173;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-NOV-1995 (first entry)
 XX
 DE Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.
 XX
 KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9507994-A2.
 XX
 PD 23-MAR-1995.
 XX
 PF 15-SEP-1994; 94WO-US010469.
 XX
 PR 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 XX
 PA (VIAG-) VIAGENE INC.
 XX
 PI Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
 XX
 DR WPI; 1995-131362/17.
 XX
 PT New alpha virus vectors for gene therapy - of viral infection, cancer,
 PT auto-immune disease, etc., and as vaccines.
 XX
 PS Example 2; Page 68; 260pp; English.
 XX
 CC The sequences given in AAQ86167-81 are primers which were used in the
 CC generation of plasmid DNA which initiates Sindbis infection. The
 CC amplified DNA sequences were used in the construction of a eukaryotic
 CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
 CC comprise a 5' sequence capable of initiating transcription of an
 CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
 CC proteins, a viral junction region which has been inactivated such that
 CC viral transcription of the subgenomic fragment is prevented, and an
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the viral
 CC junction region prevents transcription of the subgenomic fragment making
 CC vectors such as this suitable for a wide variety of applications, eg.
 CC gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX

PT like cervical cancer and viral diseases.
 PS Example 4; SEQ ID NO 37; 38pp; Chinese.
 CC A dengue virus recombinant replicon has a deletion of the complete coding
 CC sequence for preM protein of dengue virus and also includes elements of
 CC e.g. the non-coding region in the whole of the 5'-end, the coding region
 CC of the front 20 amino acids in the C protein, and the coding region of
 CC NS1 protein signal; coding regions of all non-structural proteins. The
 CC obtained vaccines are useful in producing preventives or/and remedies for
 CC cancer like cervical cancer and viral diseases. Such vaccines can
 CC efficiently express antigen in infected cells, which is because dengue
 CC virus can infect dendritic cells, and can effectively present antigen to
 CC provide immunity effect. Different types of dengue virus can be used to
 CC repeatedly produce efficient immune response thereby strengthening the
 CC body's immune system against the pathogen that contains such antigen.
 CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
 CC expressing system using of the full-length dengue virus cDNA clone
 CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
 CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
 CC lines. This sequence corresponds to an oligonucleotide used in the
 CC recombinant replicon of the invention.
 XX
 SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
 Query Match 53.3%; Score 30.4; DB 13; Length 48;
 Best Local Similarity 59.4%; Pred. No. 75;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGUNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 17 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 48
 RESULT 8
 ADT48965
 ID ADT48965 standard; DNA; 48 BP.
 XX
 AC ADT48965;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE PCR primer 5' HDVr, seq id 29.
 XX
 KW Virucide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;
 KW PCR; primer; ss.
 XX
 OS Viruses.
 XX
 PN WO2004082712-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 19-MAR-2004; 2004WO-CN000232.
 XX
 PR 20-MAR-2003; 2003CN-00115912.
 XX
 PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
 PA (TENG-) TENGGEN BIOMEDICAL CO.
 PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
 XX
 PI Pang X;
 XX
 DR WPI; 2004-699719/68.
 XX
 PT Bivalent vaccines for preventing and treating Japanese (B) encephalitis
 PT and hepatitis B produced by recombinant technique using encephalitis B
 PT virus as vector to express antigen gene of hepatitis B.
 XX
 PS Example 8; SEQ ID NO 29; 33pp; Chinese.
 XX
 CC The invention relates to a recombinant Japanese encephalitis B virus
 CC constructed from encephalitis B virus and a recombinant genome, where the

```
SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 53.3%; Score 30.4; DB 2; Length 51;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCCGCGGUNNNNNNUGGCGAUGCG 35
DB 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 10
AAQ86204
ID AAQ86204 standard; DNA; 52 BP.
XX
AC AAQ86204;
XX
XX 25-MAR-2003 (revised)
DT 23-NOV-1995 (first entry)
XX
XX Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.
DE
XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
KW transcription initiation; non-structural protein; subgenomic fragment;
KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
KW primer; polymerase chain reaction; cystic fibrosis; ss.
XX
OS Synthetic.
XX
XX WO9507994-A2.
PN
XX
XX 23-MAR-1995.
PD
XX
XX 15-SEP-1994; 94WO-US010469.
PF
XX
XX 15-SEP-1993; 93US-00122791.
PR
XX 18-FEB-1994; 94US-00198450.
PR
XX (VIAG-) VIAGENE INC.
PA
XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA,
PI Polo JM;
XX WPI; 1995-131362/17.
DR
XX New alpha virus vectors for gene therapy - of viral infection, cancer,
PT auto-immune disease, etc., and as vaccines.
PT
XX Example 7; Page 114; 260pp; English.
PS
XX The sequences given in AAQ86200-15 are primers which were used in the
CC production of alphavirus vectors expressing multiple heterologous genes.
CC These vectors are eukaryotic layered vector initiation systems (ELVIS)
CC derived from Sindbis. ELVIS's comprise a 5' sequence capable of
CC initiating transcription of an alphavirus, a nucleotide sequence encoding
CC alphavirus non-structural proteins, a viral junction region which has
CC been inactivated such that viral transcription of the subgenomic fragment
CC is prevented, and an alphavirus RNA polymerase recognition sequence.
CC Inactivation of the viral junction region prevents transcription of the
CC subgenomic fragment making vectors such as this suitable for a wide
CC variety of applications, eg. gene therapy for the treatment of cystic
CC fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCCGCGGUNNNNNNUGGCGAUGCG 35
DB 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 53.3%; Score 30.4; DB 2; Length 51;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCCGCGGUNNNNNNUGGCGAUGCG 35
DB 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 11
AAT31151
ID AAT31151 standard; DNA; 52 BP.
XX
AC AAT31151;
XX
XX 12-SEP-1996 (first entry)
DT
XX HDV reverse primer HDV17-68.
DE
XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
KW polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;
KW ribozyme; ss.
XX
OS Synthetic.
XX
XX WO9617072-A2.
PN
XX
XX 06-JUN-1996.
PD
XX
XX 30-NOV-1995; 95WO-US015490.
PF
XX
XX 30-NOV-1994; 94US-00348472.
PR
XX 18-JAN-1995; 95US-00376184.
PR
XX 15-MAR-1995; 95US-00405827.
PR
XX (CHIR ) CHIRON VIAGENE INC.
PA
XX Dubensky TW, Polo JM, Ibanez CE, Chang SM, Jolly DJ, Driver DA,
PI Belli BA;
XX
XX WPI; 1996-277785/28.
DR
XX New recombinant alpha-virus vectors - used to develop prods and methods
PT for use in gene therapy and in the prodn. of vaccines.
PT
XX Example 7; Page 120; 256pp; English.
PS
XX Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)
CC nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)
CC for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV
CC (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment
CC contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping
CC synthesis is used in a second round of PCR using primers HDV49-XC and
CC SIN276-SPE. The resulting construct contains the expression cassette
CC elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction
CC region/Sindbis structural protein genes/Sindbis 3'-end untranslated
CC region, designated pd5'26s. This was inserted into pcDNA3. Packaging cell
CC line cassettes were constructed that allow inducible expression of
CC structural proteins via alphavirus vectors
CC
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCCGCGGUNNNNNNUGGCGAUGCG 35
DB 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 12
AAT30817
ID AAT30817 standard; DNA; 52 BP.
XX
AC AAT30817;
XX
XX 12-SEP-1996 (first entry)
DT
XX HDV ribozyme primer HDV17-68.
DE
XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;
KW
```

```

KW polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;
KW hepatitis delta virus; ss.
XX
XX Synthetic.
XX
XX WO9617072-A2.
XX
XX 06-JUN-1996.
XX
XX 30-NOV-1995; 95WO-US015490.
XX
XX 30-NOV-1994; 94US-00348472.
PR 18-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00405827.
XX
XX (CHIR ) CHIRON VIAGENE INC.
XX
XX Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;
PI Beili BA;
XX
XX WPI; 1996-277785/28.
XX
XX New recombinant alpha-virus vectors - used to develop prods and methods
PT for use in gene therapy and in the prodn. of vaccines.
XX
XX Example 3; Page 85; 256pp; English.
XX
XX Primer SHDV1F (AAT30816) contains a buffer sequence allowing enzyme
CC digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme
CC sequence. It was used with nested primer HDV17-68 (AAT30817) and reverse
CC primer SHDV84R (AAT30818) to generate an HDV ribozyme. This antigenomic
CC ribozyme can be placed between the polyA tract at the 3' end of a Sindbis
CC virus-based eukaryotic layered vector initiation system, ELVIS, and the
CC transcription terminal signals to produce alphavirus expression vectors
CC useful in methods of gene therapy and for vaccine prodn
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
SQ
Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4 UCCACCUCUCCGCGGNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
RESULT 13
AAV42394
ID AAV42394 standard; DNA; 52 BP.
XX
XX AAV42394;
AC
XX 02-OCT-1998 (first entry)
DT
XX Nested PCR primer HDV17-68 of the invention.
DE
XX DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; PCR primer; ss.
XX
XX Synthetic.
OS
XX US5789245-A.
XX
XX 04-AUG-1998.
XX
XX 30-OCT-1996; 96US-00741881.
XX
XX 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
PI WPI; 1998-446089/38.
XX
XX DNA alpha:virus structural protein expression cassettes - for producing
PT recombinant alpha:virus particles.
XX
XX Example 7; Col 103; 140pp; English.
PS
XX PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC

```

CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and an
 CC alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the cell,
 CC the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 53.3%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 76;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCCUCCGCGGNNNNNNNUGGCGAUGC 35
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
 RESULT 15
 AAV60154
 ID AAV60154 standard; DNA; 52 BP.
 XX
 AC AAV60154;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 XX
 DE Nested PCR primer HDV17-68.
 XX
 KW Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis D virus.
 XX
 PN US5814482-A.
 XX
 PD 29-SEP-1998.
 XX
 PF 30-OCT-1996; 96US-00739158.
 PR 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX
 PA (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 XX
 DR WPI; 1998-541753/46.
 XX
 PT Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 PS Example 3; Col 71-72; 144pp; English.
 XX
 CC PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
 CC ribozyme sequence. The product is used in the course of the invention.
 CC The specification describes an eukaryotic layered vector initiation
 CC system, based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
 CC The RNA comprises a vector construct which autonomously amplifies in the

CC cell and expresses a heterologous nucleic acid sequence which encodes an
 CC antigen or modified form that stimulates an immune response within an
 CC animal. The system is useful for stimulating an immune response to an
 CC antigen by introducing the vector into target cells, preferably by
 CC infection in vivo, especially where the immune response is a cell
 CC mediated, HLA class I-restricted or an HLA class II-restricted immune
 CC response. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 53.3%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 76;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCCUCCGCGGNNNNNNNUGGCGAUGC 35
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
 Search completed: March 15, 2005, 11:20:07
 Job time : 319.5 secs

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:18:52 ; Search time 94.5 Seconds
(without alignments)
986.961 Million cell updates/sec

Title: US-09-699-667E-61

Perfect score: 57
Sequence: 1 ggguccaccuccucggn.....uucgcauggcuaggagacc 57

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31.8	55.8	61	1	US-08-238-963A-18
2	30.4	53.3	52	1	US-08-741-881-40
3	30.4	53.3	52	1	US-08-741-881-80
4	30.4	53.3	52	1	US-08-739-158-40
5	30.4	53.3	52	1	US-08-739-158-80
6	30.4	53.3	52	2	US-08-739-167-40
7	30.4	53.3	52	2	US-08-739-167-80
8	30.4	53.3	52	3	US-08-404-796-40
9	30.4	53.3	52	3	US-08-404-796-80
10	30.4	53.3	52	3	US-08-931-869-40
11	30.4	53.3	52	3	US-08-931-869-80
12	30.4	53.3	52	3	US-09-350-399-40
13	30.4	53.3	52	3	US-09-350-399-80
14	30.4	53.3	52	3	US-09-236-140A-40
15	30.4	53.3	52	3	US-09-236-140A-80
16	30.4	53.3	80	1	US-08-238-963A-16
17	30.4	53.3	83	3	US-08-646-695-12
18	30.4	53.3	83	5	PCT-US96-06053-12
19	30.4	53.3	84	1	US-08-238-963A-13
20	30.4	53.3	84	1	US-08-238-963A-14
21	30.4	53.3	86	1	US-08-238-963A-6
22	30.4	53.3	90	4	US-09-554-337-2
23	30.4	53.3	90	4	US-09-733-042-12
24	30.4	53.3	90	4	US-09-733-042-13
25	30.4	53.3	101	6	5225337-2
26	30.4	53.3	101	6	5225337-2
27	30.4	53.3	105	2	US-08-553-619B-25

Sequence 30, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 14046, A
Sequence 6, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 5120, Ap
Sequence 362, App
Sequence 3570, Ap
Sequence 3586, Ap
Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-238-963A-18
; Sequence 18, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,963A
; FILING DATE: May 5, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/821,155
; FILING DATE: January 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-238-963A-18

Query Match 55.8%; Score 31.8; DB 1; Length 61;
Best Local Similarity 77.4%; Pred. No. 3;
Matches 41; Conservative 6; Mismatches 2; Indels 4; Gaps 1;

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-40

Query Match 53.3%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCAUCG 35
:||||:||||:||||:||||:||||:||
DB 1 TCCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 5
US-08-739-158-80
; Sequence 80, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80

Query Match 53.3%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCAUCG 35
:||||:||||:||||:||||:||||:||
DB 1 TCCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 6
US-08-739-167-40
; Sequence 40, Application US/08739167

; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-40

Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCAUCG 35
:||||:||||:||||:||||:||||:||
DB 1 TCCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 7
US-08-739-167-80
; Sequence 80, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-80

Query Match 53.3%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||: ||
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 8
US-08-404-796-40
; Sequence 80, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-404-796-40

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||: ||
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 9
US-08-404-796-80
; Sequence 80, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-404-796-80

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||: ||
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 10
US-08-931-869-40
; Sequence 40, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-931-869-80

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps

QY 4 UCCACUCCUCGCGGUNNNNUGGCGAUCGCG 35
;||||:||||:||||:||||:||||:
DB 1 TCCACCTCCTCGCGGTCGACCTGGCGATCCG 32

RESULT 12
US-09-350-399-40
; Sequence 40, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid

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/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-350-399-40

Query Match          53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
Db 1 TCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 13
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-350-399-80

Query Match          53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
Db 1 TCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 14
US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match 53.3%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 8.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

Search completed: March 15, 2005, 15:26:33
Job time : 96.5 secs

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; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match          53.3%; Score 30.4; DB 17; Length 52;
Best Local Similarity 59.4%; Pred. No. 28;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACUCCUCCGGGNNNNNNUGGCAUGCG 35
       :||||:||||:||||:||||:||||:||||:
DB      1 TCCACCTCTCCGGCTCCGACCTGGGCATCCG 32

RESULT 3
US-10-346-880-80
; Sequence 80, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
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; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

Query Match          53.3%; Score 30.4; DB 17; Length 52;
Best Local Similarity 59.4%; Pred. No. 28;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACUCCUCCGGGNNNNNNUGGCAUGCG 35
       :||||:||||:||||:||||:||||:||||:
DB      1 TCCACCTCTCCGGCTCCGACCTGGGCATCCG 32

RESULT 4
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M
; Jolly, Douglas J
; Driver, David A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-150-407-40

Query Match          53.3%; Score 30.4; DB 17; Length 52;
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QY 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
DB 22 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 53

RESULT 9
US-10-237-302-7
; Sequence 7, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-09-06
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7

Query Match 53.3%; Score 30.4; DB 15; Length 91;
Best Local Similarity 59.4%; Pred. No. 30;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
DB 18 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 49

RESULT 10
US-10-237-302-8/c
; Sequence 8, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: AlphaVax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-09-06
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-8

Query Match 53.3%; Score 30.4; DB 15; Length 99;
Best Local Similarity 59.4%; Pred. No. 30;

Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
DB 78 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 47

RESULT 11
US-10-485-281-6
; Sequence 6, Application US/10485281
; Publication No. US20040265821A1
; GENERAL INFORMATION:
; APPLICANT: Sandig, Volker
; APPLICANT: Jordan, Ingo
; TITLE OF INVENTION: RNA Amplification System Using Plant Components in
; TITLE OF INVENTION: Animal Cells
; FILE REFERENCE: 040026us/JH
; CURRENT APPLICATION NUMBER: US/10/485,281
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: PCT/DE02/02863
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5451
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Vector p100-79
US-10-485-281-6

Query Match 53.3%; Score 30.4; DB 18; Length 5451;
Best Local Similarity 59.4%; Pred. No. 40;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
DB 5002 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 5033

RESULT 12
US-09-190-246-4
; Sequence 4, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-4

Query Match 53.3%; Score 30.4; DB 10; Length 8100;
Best Local Similarity 59.4%; Pred. No. 41;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
DB 8032 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 8063

RESULT 13
US-09-190-246-1
; Sequence 1, Application US/09190246
; Publication No. US20030180257A1

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; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15538
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-1

Query Match      53.3%; Score 30.4; DB 10; Length 15538;
Best Local Similarity 59.4%; Pred. No. 43;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACCUCUCGCGGUNNNNNNUGGCAUGCG 35
      :|||||:|||||:|||||:|||||:|||||:
Db      12479 TCACCTCTCTCGCGTCCGACCTGGGCATCCG 12510

RESULT 14
US-10-719-993-17177
; Sequence 17177, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17177
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-17177

Query Match      52.6%; Score 30; DB 18; Length 201;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 30; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY      1 GGGUCCACCUCUCGCGGUNNNNNNUGGCAUGCGUCGCAUGGCUAAGGGA 54
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Db      29 GGGAGCCCACTCGCGCGGAGAGTGGGCGAGGAGCTGAGGAAGGTACTGGA 82

RESULT 15
US-09-918-995-2716/c
; Sequence 2716, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2716
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(466)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2716

Query Match      52.6%; Score 30; DB 10; Length 466;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 23; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY      1 GGGUCCACCUCUCGCGGUNNNNNNUGGCAUGCGGCGUCGCAUGG 46
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Db      99 GGGTGTCTCTCTCGGACCTGTGCTCATGGCGCTGCGCGTGG 54

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Job time : 383.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:20:59 ; Search time 2293 Seconds
(without alignments)
946.212 Million cell updates/sec

Title: US-09-699-667E-62
Perfect score: 57
Sequence: 1 ggguccaccuccggun.....cgggcaugcuaggagccc 57

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
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2: gb_est2:*
3: gb_hic:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 3	23.6	41.4	56	8	BH638481	BH638481 1008022GO
C 4	22.8	40.0	51	8	BH413716	BH413716 1007034B0
C 5	22.2	38.9	48	9	CG777477	CG777477 1123054E1
C 6	22.2	38.9	49	1	AI956143	AI956143 wt35601.x
C 7	22.2	38.9	55	2	BE748176	BE748176 601571564
C 8	22	38.6	49	1	AA607716	AA607716 vo49b04.r
C 9	22	38.6	50	1	AU104848	AU104848 AU104848
C 10	22	38.6	51	9	CG465712	CG465712 KRIBB_2D
C 11	21.6	37.9	55	9	AL943583	AL943583 Arabidops
C 12	21.6	37.9	60	7	CV307280	CV307280 t342d08.g
C 13	21.4	37.5	46	8	BH609427	BH609427 HIV03B06
C 14	21.4	37.5	49	7	H23825	H23825 yn71e03.s1
C 15	21.4	37.5	50	1	AU107081	AU107081 AU107081
C 16	21.4	37.5	52	7	CK628443	CK628443 ip12d10.y
C 17	21.4	37.5	58	8	AZ385410	AZ385410 IM0143E22
C 18	21.2	37.2	32	7	CF296199	CF296199 30DGS--06
C 19	21.2	37.2	40	1	AA016653	AA016653 mg89g11.r
C 20	21.2	37.2	40	4	BI770067	BI770067 603053595
C 21	21.2	37.2	46	1	AI631110	AI631110 ts63e01.x
C 22	21.2	37.2	49	1	AA933587	AA933587 OF44g10.s
C 23	21.2	37.2	52	7	CV305298	CV305298 t145d06.g
C 24	21.2	37.2	58	1	AI523818	AI523818 tg96e08.x

C	25	21.2	37.2	58	1	AL878489	AL878489
C	26	21.2	37.2	58	8	BH636598	BH636598 1008012C0
C	27	21	36.8	31	1	AI688077	AI688077 wa83d03.x
C	28	21	36.8	45	9	AG194008	AG194008 Pan tregl
C	29	21	36.8	50	1	AU106032	AU106032 AU106032
C	30	21	36.8	52	1	AI092092	AI092092 qa57g07.s
C	31	20.8	36.5	43	9	CG774833	CG774833 1123021A1
C	32	20.8	36.5	48	9	CW020376	CW020376 GC0636.TI
C	33	20.8	36.5	50	9	CR021509	CR021509 Reverse s
C	34	20.8	36.5	52	8	AZ920025	AZ920025 1006017G0
C	35	20.8	36.5	54	5	BQ567053	BQ567053 gi76d12.y
C	36	20.8	36.5	58	1	AI612870	AI612870 tx20f12.x
C	37	20.8	36.5	58	8	AZ800298	AZ800298 2M0058D15
C	38	20.6	36.5	59	8	AZ499721	AZ499721 IM0337K08
C	39	20.6	36.1	43	8	AZ875350	AZ875350 2M0189M19
C	40	20.6	36.1	50	7	CN446714	CN446714 t149b03.5
C	41	20.6	36.1	50	9	CR028335	CR028335 Forward s
C	42	20.6	36.1	50	9	DR49F15T	AL984525 Danilo rer
C	43	20.6	36.1	51	8	BH641399	BH641399 1008047C1
C	44	20.6	36.1	53	9	CR002872	CR002872 Forward s
C	45	20.6	36.1	55	9	CR104304	CR104304 Reverse s

ALIGNMENTS

RESULT 1
LOCUS AA232965/c
DEFINITION zt69a04.s1 Soares NhMPu S1 Homo sapiens cDNA clone IMAGE:668622 3', similar to SW:UCRX_BOVIN_P00130 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KD PROTEIN ;, mRNA sequence.
ACCESSION AA232965
VERSION AA232965.1 GI:1856126
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 55)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubucque, T., Geisler, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 560 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source

1..55
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5562589"
/db_xref="taxon:9606"
/clone="IMAGE:668622"
/cfeature_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares NhMPu S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 2NBHM, pregnant uterus NBHU, and fetal heart NBH19W) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 47.0%; Score 26.8; DB 1; Length 55;
Best Local Similarity 48.1%; Pred. No. 1.6e+04;
Matches 26; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 3 GUCCACUCCUGCGGUNNNNUGGCAUGCCUUGCGGCAUGGCUAAGGACC 56

DB 55 GACCACATCTCGAGGGAGCGTGTGGCATCCCTCAAGCACAGTATGAGAAC 2

RESULT 2

AA878748/c 49 bp mRNA linear EST 25-MAR-1998
LOCUS of85b02.s1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:1437099 3,
DEFINITION similar to SW:YNUA_PRVKA_P33485 PROBABLE NUCLEAR ANTIGEN. ;contains
element TAR1 repetitive element ;, mRNA sequence.

ACCESSION

AA878748 GI:2987713

VERSION

AA878748.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Straubeberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

unknown library type

Trace considered overall poor quality

Seq primer: -40m13 fwd. RT from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..49

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1437099"

/tissue_type="hepatic adenoma"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Li5"

/notes="Organ: liver; Vector: pCMV-SPORT4; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 0.8 kb."

ORIGIN

Query Match 41.4%; Score 23.6; DB 1; Length 49;
Best Local Similarity 52.6%; Pred. No. 1.5e+05;
Matches 20; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCACUCCUCCUGCGGUNNNNUGGCAUGCCUUCUGGCGC 42

DB 40 CCTCTCTCCCGCGGTGGTCTTTGGGATCCCGCGCTGGC 3

RESULT 3

BH638481 56 bp DNA linear GSS 14-FEB-2002
LOCUS 1008022G07.2EL_y1 1008 - RescueMu Grid I Zea mays genomic, genomic
DEFINITION survey sequence.

ACCESSION BH638481

VERSION BH638481.1 GI:18662595

KEYWORDS

SOURCE

ORGANISM

GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 56)

AUTHORS

Walbot,V.

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008022 row: 9
Class: transposon-tagged.

FEATURES

source

1..56
Location/Qualifiers
/organism="Zea mays"
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/db_xref="taxon:4577"
/tissue_type="leaf"
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/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN

Query Match 41.4%; Score 23.6; DB 8; Length 56;
Best Local Similarity 45.7%; Pred. No. 1.5e+05;
Matches 21; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 8 CCUCCUCCUGCGGUNNNNUGGCAUGCCUUCUGGCAUGGCUAAGGG 53

DB 5 CCTCTGGTAGTGGTAGATGAGCATGGGCATGGCATGTTCACAGGG 50

RESULT 4

BH413716/c 51 bp DNA linear GSS 12-DEC-2001
LOCUS 1007034B01.2EL_xl 1007 - RescueMu Grid H Zea mays genomic, genomic
DEFINITION survey sequence.

ACCESSION BH413716

VERSION BH413716.1 GI:17590275

KEYWORDS

SOURCE

ORGANISM

GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 51)

AUTHORS

Walbot,V.

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isega,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano.S

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL ENBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
 1..50 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cloned="HRCO5037"
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ORIGIN

Query Match 38.6%; Score 22; DB 1; Length 50;
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Matches 22; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

DY
2 GGUGCCACUCGCGGCCGGUNNNNNGGCAGCUGCUCGGCAUCCC 47
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48 GTGTCCGGCTGCCGTTCGTGGGCGAACGCCAAGAGGCGGC 3

RESULT 10 CG465712/c
CG465712 LOCUS 51 bp DNA linear GSS 24-SEP-2003
DEFINITION KRIIB_2D_J77T7 pBS-TN Library Homo sapiens genomic clone
KRIIB_2D_J77 5, genomic survey sequence.
CG465712
CG465712.1 GI:35189147
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE Lee.K.T., Kim.J.H., Hahn.Y.S., Yang.J.O., Chu.M.Y., Kim.H.C., Oh.K.J., Kim.S.S., Yoo.H.S. and Kim.Y.S.

AUTHORS Rapid isolation of NotI-linked CpG island sequences from RLGS gel Unpublished (2003) Contact: KIM YS Human Genome Research Laboratory Korea Research Institute of Bioscience and Biotechnology 52 Ecoun-dong, Yusong-gu, Daeyeon 305-333, Republic of Korea Tel: 82-42-879-8110 Fax: 82-42-879-8119 Email: yongsang@kribb.re.kr This result was produced by the program for Functional Analysis of Human Genome funded from Ministry of Science and Technology, Republic of Korea. Clones are available from the Center for Functional Analysis of Human Genome. See URL:
<http://21cgenome.kribb.re.kr/> for details or contact: yongsang@kribb.re.kr.

TITLE Seq primer: T7 primer Class: NotI site High quality sequence stop: 5l.

JOURNAL Location/Qualifiers COMMENT 1..51 /organism="Homo sapiens"


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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Okubo,K.,
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
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/mol_type="mRNA"
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/clone="HRC06015"
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Best Local Similarity 48.7%; Pred. No. 7e+05;
Matches 19; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 14 CCGCGUNNNNUGGCAUGCCUUGCGGCAUGGCUAAGG 52
Db 47 CTCGGTGGAGCCGGGGCCGGTGTTCGGTAGGGGAGG 9
Search completed: March 15, 2005, 20:38:08
Job time : 2299 secs

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		Match	Length			
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2	47.4	83.2	57	6	AX012282	Sequence
3	47.4	83.2	57	6	AX012283	Sequence
4	47.4	83.2	57	6	AX012285	Sequence
5	47.4	83.2	57	6	AX012286	Sequence
6	47.4	83.2	57	6	AX012287	Sequence
7	47.4	83.2	57	6	AX012288	Sequence
8	47.4	83.2	57	6	AX012289	Sequence
9	47.4	83.2	57	6	AX012290	Sequence
10	34.6	60.7	144620	9	AC023787	Homo sapi
11	34.2	60.0	197752	2	AC145130	Homo sapi
12	34	59.6	37	6	AX012291	Sequence
13	32.8	57.5	60721	9	BX321878	Human DNA
C 14	32.2	56.5	267	6	BD060287	Secreted
C 15	32.2	56.5	440	6	CQ695370	Sequence
C 16	32.2	56.5	1340	9	BC003411	Homo sapi
C 17	32.2	56.5	1404	6	AX540424	Sequence
C 18	32.2	56.5	1540	6	CQ722745	Sequence
C 19	32.2	56.5	1927	6	AR339235	Sequence

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
Nucleic acid enzyme for rna cleavage
Patent: WO 995856-A 44 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
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/note="synthetic nucleic acid"
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Best Local Similarity 64.9%; Pred. No. 0.57;
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RESULT 3
AX012283
LOCUS
AX012283
DEFINITION
Sequence 45 from Patent WO995856.
ACCESSION
AX012283.1 GI:9998344
VERSION
AX012283.1
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 45 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;
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Db 1 GGGTCCACCTCTCGCGGTCCGACGTCGGCATCGGCTTCGCATGCTAAGGACCC 57
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RESULT 4
AX012285
LOCUS
AX012285
DEFINITION
Sequence 47 from Patent WO995856.
ACCESSION
AX012285
VERSION
AX012285.1 GI:9998346
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 47 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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/note="synthetic nucleic acid"
ORIGIN
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Best Local Similarity 64.9%; Pred. No. 0.57;
Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;
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Db 1 GGGTCCACCTCTCGCGGTCCGACGTCGGCATCGGCTTCGCATGCTAAGGACCC 57
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RESULT 5
AX012286
LOCUS
AX012286
DEFINITION
Sequence 48 from Patent WO995856.
ACCESSION
AX012286
VERSION
AX012286.1 GI:9998347
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 48 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Best Local Similarity 64.9%; Pred. No. 0.57;
Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;
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RESULT 6
AX012287
LOCUS
AX012287
DEFINITION
Sequence 49 from Patent WO995856.
ACCESSION
AX012287
VERSION
AX012287.1 GI:9998348
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 49 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Location/Qualifiers
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Best Local Similarity 64.9%; Pred. No. 0.57;
Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

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Db 1 GGGTCCACCTCTCGCGGCTCCGAGTGGGCGATCGGGCTTCGCATGGCTAAGGGACCC 57

RESULT 7
AX012288
LOCUS      AX012288
DEFINITION Sequence 50 from Patent WO9955856.
ACCESSION  AX012288
VERSION     AX012288.1 GI:9998349
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE       Nucleic acid enzyme for rna cleavage
JOURNAL     Patent: WO 9955856-A 50 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES    Location/Qualifiers
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               /organism="synthetic construct"
               /mol_type="unassigned RNA"
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               /note="synthetic nucleic acid"
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Query Match      83.2%; Score 47.4; DB 6; Length 57;
Best Local Similarity 64.9%; Pred. No. 0.57;
Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGUCCACCTCTCGCGGCTCCGAGTGGGCGATCGGGCTTCGCATGGCTAAGGGACCC 57
Db 1 GGGTCCACCTCTCGCGGCTCCGAGTGGGCGATCGGGCTTCGCATGGCTAAGGGACCC 57

RESULT 8
AX012289
LOCUS      AX012289
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION  AX012289
VERSION     AX012289.1 GI:9998350
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE       Nucleic acid enzyme for rna cleavage
JOURNAL     Patent: WO 9955856-A 51 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES    Location/Qualifiers
             source
               1..57
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               /note="synthetic nucleic acid"
ORIGIN
Query Match      83.2%; Score 47.4; DB 6; Length 57;
Best Local Similarity 64.9%; Pred. No. 0.57;
Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGUCCACCTCTCGCGGCTCCGAGTGGGCGATCGGGCTTCGCATGGCTAAGGGACCC 57
Db 1 GGGTCCACCTCTCGCGGCTCCGAGTGGGCGATCGGGCTTCGCATGGCTAAGGGACCC 57

RESULT 9
AX012290
LOCUS      AX012290
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION  AX012290
VERSION     AX012290.1 GI:9998351
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE       Nucleic acid enzyme for rna cleavage
JOURNAL     Patent: WO 9955856-A 52 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES    Location/Qualifiers
             source
               1..57
               /organism="synthetic construct"
               /mol_type="unassigned RNA"
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               /note="synthetic nucleic acid"
ORIGIN
Query Match      83.2%; Score 47.4; DB 6; Length 57;
Best Local Similarity 64.9%; Pred. No. 0.57;
Matches 37; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGUCCACCTCTCGCGGCTCCGAGTGGGCGATCGGGCTTCGCATGGCTAAGGGACCC 57
Db 1 GGGTCCACCTCTCGCGGCTCCGAGTGGGCGATCGGGCTTCGCATGGCTAAGGGACCC 57

RESULT 10
AX023787
LOCUS      AX023787
DEFINITION Homo sapiens BAC clone RP11-546M8 from 2, complete sequence.
ACCESSION  AC023787
VERSION     AC023787.8 GI:16306517
KEYWORDS   HTG.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 144620)
AUTHORS     Sulston,J.E. and Waterston,R.
TITLE       Toward a complete human genome sequence
JOURNAL     Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE     99063792
PUBMED      9847074
REFERENCE   2 (bases 1 to 144620)
AUTHORS     Du,F., Haakenson,W., Doeber,A. and Boyer,E.
TITLE       The sequence of Homo sapiens BAC clone RP11-546M8
JOURNAL     Unpublished (2001)
REFERENCE   3 (bases 1 to 144620)
AUTHORS     Waterston,R.H.
TITLE       Direct Submission
JOURNAL     Submitted (17-FEB-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4 (bases 1 to 144620)
AUTHORS     Waterston,R.H.
TITLE       Direct Submission
JOURNAL     Submitted (22-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5 (bases 1 to 144620)
AUTHORS     Waterston,R.H.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2001) Genome Sequencing Center, Washington
```

University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 6 (bases 1 to 144620)
 Waterston, R.
 Direct Submission
 Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Oct 22, 2001 this sequence version replaced gi:15487510.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.edu
 ----- Summary Statistics

 Center project name: H_NH0546M08

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenken, E., Tateno, M., Cacanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-110K9, 2000 bp overlap; the clone sequenced to the right is RP11-314A6. Actual start of this clone is at base position 161607 of RP11-110K9; actual end is at base position 144620 of RP11-546M8.

Data from AC079612 was used to finish this clone, AC023787. Polymorphisms have been identified between AC079612, AC062017, and AC023787.

FEATURES

source

Location/Qualifiers

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 /db_xref="taxon:9606"
 /chromosome="2"
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 162..1004
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 1065..1559
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 1560..2052
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 2053..2102
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 2353..2373

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region
 2354..2659
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 3170..3948
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 8374..8405
 /rpt_family="(CA)n"
 9718..10023
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 9995..10043
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 10031..10045
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 10046..10364
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 10164..10185
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 10338..10358
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 10365..10547
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 10518..10558
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 10906..11034
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 12055..12359
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 12337..12356
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 12398..12420
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 12810..13145
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 14255..14307
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Query Match      60.7%; Score 34.6; DB 9; Length 144620;
Best Local Similarity 50.9%; Pred. No. 1.5e+02;
Matches 29; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

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QY 1 GGUCCACCUCCUGCGGUNNNNUGGCAUGCCUUGCGGCAUGGCUAAGGACCC 57
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76297 GGTTCAGCTCTCTCGGGAGCCCCCTGCTCATGCTGAGTGCTGCTCAGGCACAC 76353

```

RESULT 11

```

AC145130
LOCUS      AC145130               197752 bp    DNA    linear    HTG 10-JUN-2003
DEFINITION Homo sapiens chromosome 5 clone RP11-109017, WORKING DRAFT
SEQUENCE. 51 unordered pieces.
AC145130
VERSION    AC145130.1 GI:31560121
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 197752)
AUTHORS    DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 5
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 197752)
AUTHORS    DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (10-JUN-2003) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT    -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----
            Project Information
            Center Project Name: 448574
            Center clone name: RPCI-11_109017
            -----
            Summary Statistics
            Consensus quality: 176983 bases at least Q40
            Consensus quality: 181876 bases at least Q30
            Consensus quality: 186025 bases at least Q20
            Estimated insert size: 175000; agarose-fp estimation
            Quality coverage: 5.72 in Q20 bases; agarose-fp estimation
            Quality coverage: 5.19 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 51 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence

```

```

* as soon as it is available and the accession number will
* be preserved.

```

```

1 1094: contig of 1094 bp in length
1095: gap of unknown length
1195: contig of 1503 bp in length
2698: gap of unknown length
2798: contig of 1590 bp in length
4388: gap of unknown length
4488: contig of 1385 bp in length
5873: gap of unknown length
5973: contig of 1044 bp in length
7017: gap of unknown length
7117: contig of 1424 bp in length
8541: gap of unknown length
8641: contig of 1706 bp in length
10347: gap of unknown length
12316: contig of 1869 bp in length
12316: gap of unknown length
12416: contig of 1924 bp in length
14340: gap of unknown length
14440: contig of 2786 bp in length
17226: gap of unknown length
17326: contig of 1246 bp in length
18572: gap of unknown length
18672: contig of 1790 bp in length
20462: gap of unknown length
20562: contig of 1681 bp in length
22342: gap of unknown length
23308: contig of 1566 bp in length
24008: gap of unknown length
26508: contig of 2500 bp in length
26608: gap of unknown length
28562: contig of 1954 bp in length
28662: gap of unknown length
31029: contig of 2367 bp in length
31129: gap of unknown length
33167: contig of 2038 bp in length
33267: gap of unknown length
35738: contig of 2471 bp in length
35838: gap of unknown length
37891: contig of 2053 bp in length
37991: gap of unknown length
41055: contig of 3064 bp in length
41155: gap of unknown length
42773: contig of 1618 bp in length
42873: gap of unknown length
45089: contig of 2216 bp in length
45189: gap of unknown length
47079: contig of 1890 bp in length
47179: gap of unknown length
49683: contig of 2504 bp in length
49783: gap of unknown length
53085: contig of 3302 bp in length
53185: gap of unknown length
55662: contig of 2477 bp in length
55762: gap of unknown length
58111: contig of 2349 bp in length
58211: gap of unknown length
60308: contig of 1997 bp in length
60308: gap of unknown length
63834: contig of 3526 bp in length
63934: gap of unknown length
66924: contig of 2990 bp in length
67024: gap of unknown length
69559: contig of 2535 bp in length
69559: gap of unknown length
73243: contig of 3584 bp in length
73243: gap of unknown length
78064: contig of 4721 bp in length
78164: gap of unknown length
81521: contig of 3357 bp in length
81621: gap of unknown length
85647: contig of 4026 bp in length

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* 85648 85747: gap of unknown length
* 85748 89153: contig of 3406 bp in length
* 89154 89253: gap of unknown length
* 89254 96627: contig of 7374 bp in length
* 96628 96727: gap of unknown length
* 96728 102006: contig of 5279 bp in length
* 102007 102106: gap of unknown length
* 102107 106742: contig of 4636 bp in length
* 106743 106842: gap of unknown length
* 106843 112687: contig of 5845 bp in length
* 112688 112788: gap of unknown length
* 112788 118426: contig of 5639 bp in length
* 118427 118526: gap of unknown length
* 118527 124506: contig of 5980 bp in length
* 124507 124606: gap of unknown length
* 124607 130739: contig of 6133 bp in length
* 130740 130839: gap of unknown length
* 130840 137824: contig of 6985 bp in length
* 137825 137925: gap of unknown length
* 137925 144946: contig of 7022 bp in length
* 144947 145047: gap of unknown length
* 145047 153777: contig of 8731 bp in length
* 153778 153877: gap of unknown length
* 153878 162704: contig of 8827 bp in length
* 162705 162804: gap of unknown length
* 162805 171863: contig of 9059 bp in length
* 171864 171964: gap of unknown length
* 171964 183850: contig of 11886 bp in length
* 183850 183949: gap of unknown length
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    Matches 29; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCGAUGCCUUCGCGAUGGCUAAGGAC 55
Db 53018 GTGACAGCTCCTTGAGAGCTCCATGGGCGATGGCTATGGCGCATGAAGGAC 53072

RESULT 12
AX012291
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DEFINITION
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VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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            Nucleic acid enzyme for rna cleavage
            Patent: WO 995856-A 53 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
            Location/Qualifiers
                1..37
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    Matches 23; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCGAUGCCUUCGCGGCAU 44

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Best Local Similarity 64.7%; Pred. No. 2.3e+03;
Matches 22; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGTCCACCTCTCGGGTCCGACCTGGCGCATGC 34

RESULT 13
BX321878/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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ORIGIN
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    Best Local Similarity 52.3%; Pred. No. 5.9e+02;
    Matches 23; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCGAUGCCUUCGCGGCAU 44

```

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl>

XXYac-13Cf11 is from the ICI Human YAC library (RA) VECTOR: pYAC4.

[illegible]

RESULT 14	BD060287	267 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD060287/c				
DEFINITION	Scrated expressed sequence tags (sESTs).				
ACCESSION	BD060287				
VERSION	BD060287.1	GI:22605893			
KEYWORDS	JP 2001518793-A/647.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 267) Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D., Treacy,M., Spaulding,V. and Agostino,M.J.				
TITLE	Scrated expressed sequence tags (sESTs)				
JOURNAL	Patent: JP 2001518793-A 647 16-OCT-2001; GENETICS INSTITUTE INC				
COMMENT	PN JP 2001518793-A/647 PD 16-OCT-2001 PF 10-APR-1998 JP 1998543070 PR 10-APR-1997 US 08/837312 PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE,PI DAVID MERBERG, PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers.				

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Db     172 GTGACAGCTTCCTTGAGAAGCTCATCGGTATGCTATGCGTATGGCTTAAGG    120
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RESULT 15
CQ695370/c
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/db_xref="taxon:9606"

CQ695370
Sequence 40296 from Patent WO02070737.
CQ695370
CQ695370.1 GI:42241732
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
Liew, C.C., Marshall, W.E. and Zhang, H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 40296 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
1. 440
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/db_xref="taxon:9606"

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Query Match

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:59:13 ; Search time 376.5 Seconds
(without alignments)
900.574 Million cell updates/sec

Title: US-09-699-667E-62

Perfect score: 57
Sequence: 1 ggguccaccucccggn.....cgggaugcuaaggagacc 57

Scoring table: IDENTITY NUCDX

Gapop 10_0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCT05_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32.2	56.5	267	13	US-10-040-739-647 Sequence 647, App
C 2	32.2	56.5	440	17	US-10-242-535A-40296 Sequence 40296, A
C 3	32.2	56.5	440	17	US-10-085-783A-40296 Sequence 40296, A
C 4	32.2	56.5	1404	17	US-10-466-164-36 Sequence 36, Appl
C 5	32.2	56.5	1430	15	US-10-106-698-605 Sequence 605, App
C 6	32.2	56.5	1430	17	US-10-264-237-853 Sequence 853, App
C 7	32.2	56.5	1927	15	US-10-037-270-726 Sequence 726, App
C 8	32.2	56.5	1927	17	US-10-117-722-726 Sequence 726, App
C 9	32.2	56.5	2206	11	US-09-764-875-185 Sequence 185, App
C 10	32.2	56.5	2298	15	US-10-176-306-27 Sequence 27, Appl
C 11	32.2	56.5	2519	13	US-10-139-262-9 Sequence 9, Appl

C 12	32.2	56.5	2519	14	US-10-255-969-9 Sequence 9, Appl
C 13	32.2	56.5	2700	14	US-10-028-072-27 Sequence 27, Appl
C 14	32.2	56.5	2700	14	US-10-140-808-27 Sequence 27, Appl
C 15	32.2	56.5	2700	14	US-10-121-049-27 Sequence 27, Appl
C 16	32.2	56.5	2700	14	US-10-123-904-27 Sequence 27, Appl
C 17	32.2	56.5	2700	14	US-10-140-470-27 Sequence 27, Appl
C 18	32.2	56.5	2700	14	US-10-175-746-27 Sequence 27, Appl
C 19	32.2	56.5	2700	14	US-10-176-918-27 Sequence 27, Appl
C 20	32.2	56.5	2700	14	US-10-176-921-27 Sequence 27, Appl
C 21	32.2	56.5	2700	14	US-10-137-865-27 Sequence 27, Appl
C 22	32.2	56.5	2700	14	US-10-140-474-27 Sequence 27, Appl
C 23	32.2	56.5	2700	14	US-10-142-431-27 Sequence 27, Appl
C 24	32.2	56.5	2700	14	US-10-143-114-27 Sequence 27, Appl
C 25	32.2	56.5	2700	14	US-10-142-419-27 Sequence 27, Appl
C 26	32.2	56.5	2700	14	US-10-123-262-27 Sequence 27, Appl
C 27	32.2	56.5	2700	14	US-10-142-423-27 Sequence 27, Appl
C 28	32.2	56.5	2700	14	US-10-121-050-27 Sequence 27, Appl
C 29	32.2	56.5	2700	14	US-10-141-755-27 Sequence 27, Appl
C 30	32.2	56.5	2700	14	US-10-143-032-27 Sequence 27, Appl
C 31	32.2	56.5	2700	14	US-10-123-108-27 Sequence 27, Appl
C 32	32.2	56.5	2700	14	US-10-123-236-27 Sequence 27, Appl
C 33	32.2	56.5	2700	14	US-10-123-261-27 Sequence 27, Appl
C 34	32.2	56.5	2700	14	US-10-140-921-27 Sequence 27, Appl
C 35	32.2	56.5	2700	14	US-10-140-938-27 Sequence 27, Appl
C 36	32.2	56.5	2700	14	US-10-121-045-27 Sequence 27, Appl
C 37	32.2	56.5	2700	14	US-10-123-292-27 Sequence 27, Appl
C 38	32.2	56.5	2700	14	US-10-123-903-27 Sequence 27, Appl
C 39	32.2	56.5	2700	14	US-10-124-819-27 Sequence 27, Appl
C 40	32.2	56.5	2700	14	US-10-124-822-27 Sequence 27, Appl
C 41	32.2	56.5	2700	14	US-10-140-935-27 Sequence 27, Appl
C 42	32.2	56.5	2700	14	US-10-160-498-27 Sequence 27, Appl
C 43	32.2	56.5	2700	14	US-10-124-824-27 Sequence 27, Appl
C 44	32.2	56.5	2700	14	US-10-127-825A-27 Sequence 27, Appl
C 45	32.2	56.5	2700	14	US-10-127-829A-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-10-040-739-647/c
; Sequence 647, Application US/10040739
; Publication No. US20020173635A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John
; LaVallie, Edward
; Racie, Lisa
; Merberg, David
; Treacy, Maurice
; Spaulding, Vikki
; TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
; NUMBER OF SEQUENCES: 1519
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/040,739
; FILING DATE: 07-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/036,520
; FILING DATE: 03-JUN-1998
; ATTORNEY/AGENT INFORMATION:

```
/ NAME: Brown, Scott A.
/ REGISTRATION NUMBER: 32,724
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 498-8224
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 647:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 647:
US-10-040-733-647

Query Match          56.5%; Score 32.2; DB 13; Length 267;
Best Local Similarity 50.9%; Pred. No. 8.6;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGAUGCCUUCGCGGAUGGCUAAGG 53
Db 172 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGGCATGGCTAAAG 120

RESULT 2
US-10-242-535A-40296/c
; Sequence 40296, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40296
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (361)..(361)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (369)..(369)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (371)..(371)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-40296

Query Match          56.5%; Score 32.2; DB 17; Length 440;
Best Local Similarity 50.9%; Pred. No. 8.9;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGAUGCCUUCGCGGAUGGCUAAGG 53
Db 259 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGGCATGGCTAAAG 207

RESULT 3
US-10-085-783A-40296/c
; Sequence 40296, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40296
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (369)..(369)
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US-10-085-783A-40296

Query Match          56.5%; Score 32.2; DB 17; Length 440;
Best Local Similarity 50.9%; Pred. No. 8.9;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCGAUGCCUUCGCGGAUGGCUAAGG 53
Db 259 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGGCATGGCTAAAG 207

RESULT 4
US-10-466-164-36/c
; Sequence 36, Application US/10466164
; Publication No. US20040058365A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; PANZER, Scott R.;
; APPLICANT: LINCOLN, Stephen E.; ALTUS, Christina M.;
; APPLICANT: DUFOUR, Gerard E.; JACKSON, Jennifer L.;
; APPLICANT: JONES, Anissa L.; DAM, Tam C.;
; APPLICANT: LIU, Tommy F.; HARRIS, Bernard;
; APPLICANT: FLORES, Vincent Z.; DAFO, Abel;
; APPLICANT: MARWAHA, Rakeeh; CHEN, Alice J.;
; APPLICANT: CHANG, Simon C.; GERSTIN, Jr., Edward H.;
; APPLICANT: PERALTA, Careyana H.; DAVID, Marie H.;
; APPLICANT: LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1215 PCT
; CURRENT APPLICATION NUMBER: US/10/466,164
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/US02/01008
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; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/263,065
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/263,329
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/262,209
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,326
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,063
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inceyte ID No. US20040058365A1 LI:199716.6:2001JAN12
US-10-466-164-36

Query Match 56.5%; Score 32.2; DB 17; Length 1404;
Best Local Similarity 50.9%; Pred. No. 9.7;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUGCCUUCGGCAUGGCUAAGG 53
DB 799 GTGACAGCTTCTTGAGAGCTCCATGGCATGGCTATGGCATGGCTAAAGG 747

RESULT 5
US-10-106-698-605/c
; Sequence 605, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 605
; LENGTH: 1430
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-605

Query Match 56.5%; Score 32.2; DB 15; Length 1430;
Best Local Similarity 50.9%; Pred. No. 9.7;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUGCCUUCGGCAUGGCUAAGG 53
DB 98 GTGRCAGCTTCTTGAGAGCTCCATGGCATGGCTATGGCATGGCTAAAGG 46

RESULT 6
US-10-264-237-853/c
; Sequence 853, Application US/10264237

; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 853
; LENGTH: 1430
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-853

Query Match 56.5%; Score 32.2; DB 17; Length 1430;
Best Local Similarity 50.9%; Pred. No. 9.7;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUGCCUUCGGCAUGGCUAAGG 53
DB 98 GTGRCAGCTTCTTGAGAGCTCCATGGCATGGCTATGGCATGGCTAAAGG 46

RESULT 7
US-10-037-270-726/c
; Sequence 726, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 726
; LENGTH: 1927
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1224)
US-10-037-270-726

Query Match 56.5%; Score 32.2; DB 15; Length 1927;
Best Local Similarity 50.9%; Pred. No. 9.9;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

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QY 1 GGUCCACCUCCUGCGGUNNNNNUGGCAUGCCUUCGCGCAUGGCUAAGG 53
Db 594 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGGCATGCTAAAGG 542

RESULT 8
US-10-117-722-726/c
; Sequence 726, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20030219744A1e1 Nucleic Acids and
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 726
; LENGTH: 1927
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: (88)..(1224)
US-10-117-722-726

Query Match 56.5%; Score 32.2; DB 17; Length 1927;
Best Local Similarity 50.9%; Pred. No. 9.9;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGUNNNNNUGGCAUGCCUUCGCGCAUGGCUAAGG 53
Db 594 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGGCATGCTAAAGG 542

RESULT 9
US-09-764-875-185/c
; Sequence 185, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 185
; LENGTH: 2206
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-875-185

Query Match 56.5%; Score 32.2; DB 11; Length 2206;
Best Local Similarity 50.9%; Pred. No. 10;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGUNNNNNUGGCAUGCCUUCGCGCAUGGCUAAGG 53
Db 884 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGGCATGCTAAAGG 832
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RESULT 10
US-10-176-306-27/c
; Sequence 27, Application US/10176306
; Publication No. US20030130485A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL HUMAN GENES AND METHODS OF USE THEREOF
; FILE REFERENCE: 10448-195001
; CURRENT APPLICATION NUMBER: US/10/176,306
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/001,137
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/45291
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/248,362
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/248,331
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/248,365
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/250,077
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,327
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,176
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 10/023,617
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/49416
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,249
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,405
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 10/083,248
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: PCT/US01/46717
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,324
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,518
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/241,989
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-176-306-27

Query Match 56.5%; Score 32.2; DB 15; Length 2298;
Best Local Similarity 50.9%; Pred. No. 10;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGUNNNNNUGGCAUGCCUUCGCGCAUGGCUAAGG 53
Db 1668 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGGCATGCTAAAGG 1616

RESULT 11
US-10-139-262-9/c
; Sequence 9, Application US/10139262
; Publication No. US20020128459A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YUSUKE
```


APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/139,262
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US/09/380,287A
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62259
PRIOR FILING DATE: 1997-02-28
PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 2519
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1785)
FEATURE:
NAME/KEY: misc feature
LOCATION: (289)..(291)
OTHER INFORMATION: xaa is Phe or Leu
FEATURE:
NAME/KEY: misc feature
LOCATION: (1015)..(1017)
OTHER INFORMATION: xaa is Lys or Arg
FEATURE:
NAME/KEY: misc feature
LOCATION: (1492)..(1494)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1609)..(1611)
OTHER INFORMATION: xaa is Gln or Lys or Glu
FEATURE:
NAME/KEY: misc feature
LOCATION: (2493_2516)
OTHER INFORMATION: n is a or g or c or t
US-10-139-262-9

Query Match 56.5%; Score 32.2; DB 13; Length 2519;
Best Local Similarity 50.9%; Pred. No. 10;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACUCCUCCGCGGNNNNNUGGCGCAUGCCUUCGGGCAUGGCUAAGG 53
DB 1155 GTGACAGCTTCTTGAGAAGCTCCATGGCGCATGCTATGGCGCTAAAGG 1103

RESULT 12
US-10-255-969-9/c
Sequence 9, Application US/10255969
Publication No. US20030083486A1
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: TANAKA, TOSHIHIRO
APPLICANT: TSUKADA, SHUICHI
TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE PROTEIN ORIGINATING IN MAMMALS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/255,969
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US/09/380,287
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: JP 1997-62259
PRIOR FILING DATE: 1997-02-28

PRIOR APPLICATION NUMBER: JP 1998-62263
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 2519
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1785)
FEATURE:
NAME/KEY: misc feature
LOCATION: (289)..(291)
OTHER INFORMATION: xaa is Phe or Leu
FEATURE:
NAME/KEY: misc feature
LOCATION: (1015)..(1017)
OTHER INFORMATION: xaa is Lys or Arg
FEATURE:
NAME/KEY: misc feature
LOCATION: (1492)..(1494)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1609)..(1611)
OTHER INFORMATION: xaa is Gln or Lys or Glu
FEATURE:
NAME/KEY: misc feature
LOCATION: (2493_2516)
OTHER INFORMATION: n is a or g or c or t
US-10-255-969-9

Query Match 56.5%; Score 32.2; DB 14; Length 2519;
Best Local Similarity 50.9%; Pred. No. 10;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACUCCUCCGCGGNNNNNUGGCGCAUGCCUUCGGGCAUGGCUAAGG 53
DB 1155 GTGACAGCTTCTTGAGAAGCTCCATGGCGCATGCTATGGCGCTAAAGG 1103

RESULT 13
US-10-028-072-27/c
Sequence 27, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match 56.5%; Score 32.2; DB 14; Length 2700;
Best Local Similarity 50.9%; Pred. No. 10;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUCCUUGCGGCAUGGCUAAGG 53
DB 1886 GTGACAGCTTCCTTGAGAAGCTCCATGGCGCATGGCTATGGCGTAAAGG 1834

RESULT 14
US-10-140-808-27/c
; Sequence 27, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140, 808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 27
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-140-808-27

Query Match 56.5%; Score 32.2; DB 14; Length 2700;
Best Local Similarity 50.9%; Pred. No. 10;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUCCUUGCGGCAUGGCUAAGG 53
DB 1886 GTGACAGCTTCCTTGAGAAGCTCCATGGCGCATGGCTATGGCGTAAAGG 1834

RESULT 15
US-10-121-049-27/c
; Sequence 27, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121, 049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 27
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-121-049-27

Query Match 56.5%; Score 32.2; DB 14; Length 2700;
Best Local Similarity 50.9%; Pred. No. 10;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUCCUUGCGGCAUGGCUAAGG 53
DB 1886 GTGACAGCTTCCTTGAGAAGCTCCATGGCGCATGGCTATGGCGTAAAGG 1834

Search completed: March 15, 2005, 15:51:54
Job time : 379.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:06:47 ; Search time 2476.25 Seconds
(without alignments)
876.189 Million cell updates/sec

Title: US-09-699-667E-62
Perfect score: 57
Sequence: 1 ggguccaccuccggun.....cgggcaugcuaggagacc 57

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33.8	59.3	997	1	AL558230	AL558230 AL558230
2	32.2	56.5	191	2	BE939096	BE939096 PM2-TN012
3	32.2	56.5	323	4	BF993112	BF993112 PM1-GN006
4	32.2	56.5	329	2	BF377686	BF377686 PM2-TN012
5	32.2	56.5	331	4	BF955707	BF955707 PM1-GN006
C 6	32.2	56.5	474	1	AA134752	AA134752 Z119A11.1
C 7	32.2	56.5	474	1	AU128462	AU128462 AU128462
C 8	32.2	56.5	550	5	BP379433	BP379433 BP379433
C 9	32.2	56.5	555	2	BE541011	BE541011 601064357
C 10	32.2	56.5	581	5	BP207776	BP207776 BP207776
C 11	32.2	56.5	583	5	BP222743	BP222743 BP222743
C 12	32.2	56.5	635	6	CB123548	CB123548 K-EST0171
C 13	32.2	56.5	639	7	CK001771	CK001771 AGENCOURT
C 14	32.2	56.5	667	2	BF031657	BF031657 601558148
C 15	32.2	56.5	671	5	BU657400	BU657400 C123002.2
C 16	32.2	56.5	680	7	CN310414	CN310414 170006001
C 17	32.2	56.5	708	4	BM718340	BM718340 UI-E-E01-
C 18	32.2	56.5	859	2	BF694284	BF694284 602082921
C 19	32.2	56.5	863	5	BQ440211	BQ440211 AGENCOURT
C 20	32.2	56.5	866	5	BQ438983	BQ438983 AGENCOURT
C 21	32.2	56.5	879	6	CA454195	CA454195 AGENCOURT
C 22	32.2	56.5	883	2	BP214247	BP214247 601848430
C 23	32.2	56.5	922	7	CO649188	CO649188 ILLUMIGEN
C 24	32.2	56.5	929	5	BX329141	BX329141

C 25	32.2	56.5	936	2	BE871943	BE871943 601447974
C 26	32.2	56.5	963	7	CO581585	CO581585 ILLUMIGEN
C 27	32.2	56.5	991	4	BM564843	BM564843 AGENCOURT
C 28	32.2	56.5	1851	9	AY413214	AY413214 Homo sapi
C 29	32.2	56.5	1851	9	AY413215	AY413215 Pan trogl
C 30	32.2	56.5	2175	3	CR592705	CR592705 full-leng
C 31	32.2	56.5	2175	3	BB822907	BB822907 BB822907
C 32	31.6	55.4	484	6	CB515365	CB515365 89a1r9b51
C 33	31.6	55.4	504	6	CA651173	CA651173 wreln.pk1
C 34	31.4	55.1	953	5	BQ722008	BQ722008 AGENCOURT
C 35	31	54.4	498	1	AI176901	AI176901 EST220507
C 36	31	54.4	791	8	CC441411	CC441411 PUFNF817B
C 37	31	54.4	1009	5	BUS12545	BUS12545 AGENCOURT
C 38	31	54.4	1097	5	BE923378	BE923378 AGENCOURT
C 39	30.6	53.7	401	2	BE712520	BE712520 QV2-HT069
C 40	30.4	53.3	352	6	CB461354	CB461354 721312 MA
C 41	30.4	53.3	440	1	AV618833	AV618833 AV618833
C 42	30.4	53.3	505	4	BI535252	BI535252 398661 MA
C 43	30.4	53.3	528	7	CK970752	CK970752 4086214 B
C 44	30.4	53.3	538	4	BM839521	BM839521 K-EST0116
C 45	30.4	53.3	574	4	BM185653	BM185653 fv74c01.y

ALIGNMENTS

RESULT 1
LOCUS AL558230 997 bp mRNA linear EST 02-APR-2004
DEFINITION AL558230 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION Homo sapiens cDNA clone CS0DJ001YN05 3-PRIME, mRNA sequence.
VERSION AL558230
KEYWORDS EST.
SOURCE AL558230.3 GI:46183629
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 997)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31280029.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3461.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DJ001C03NP1&c=3461.f.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 59.3%; Score 33.8; DB 1; Length 997;
Best Local Similarity 50.9%; Pred. No. 1.7e+02;

Matches 28; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GGUCCACCUCCUGCGGNNNNUGGCAUGCCUUCGGCAUGGCUAAGGAC 55
Db 778 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGCATGCTAAAGMC 832

RESULT 2
BE939096
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BE939096 191 bp mRNA linear EST 02-OCT-2000
PM2-TN0123-300800-001-b12 TN0123 Homo sapiens cDNA, mRNA sequence.
BE939096
VERSION
KEYWORDS
SOURCE
ORGANISM

BE939096.1 GI:10467120
Homo sapiens (human)

REFERENCE
AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
PUBMED
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2-TN0123-300800-001-b12&t3=2000-08-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 4
High quality sequence stop: 190.

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0123"
/note="Organ: testis_normal; Vector: puc18; Site_1: Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 56.5%; Score 32.2; DB 2; Length 191;
Best Local Similarity 50.9%; Pred. No. 4.3e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GGUCCACCUCCUGCGGNNNNUGGCAUGCCUUCGGCAUGGCUAAGG 53
Db 115 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGCATGCTAAAGG 167

RESULT 3
BF993112
LOCUS

BF993112 323 bp mRNA linear EST 23-JAN-2001

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

PM1-GN0066-311000-001-g08 GN0066 Homo sapiens cDNA, mRNA sequence.
BF993112
VERSION
KEYWORDS
SOURCE
ORGANISM

BF993112.1 GI:12399435
Homo sapiens (human)

REFERENCE
AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
PUBMED
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1-GN0066-311000-001-g08&t3=2000-10-31&t4=1)
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High quality sequence start: 67
High quality sequence stop: 322.

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/dev_stage="Adult"
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/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 56.5%; Score 32.2; DB 4; Length 323;
Best Local Similarity 50.9%; Pred. No. 4.5e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GGUCCACCUCCUGCGGNNNNUGGCAUGCCUUCGGCAUGGCUAAGG 53
Db 134 GTGACAGCTTCCTTGAGAGCTCCATGGGCATGGCTATGGCATGCTAAAGG 186

RESULT 4
BF377686
LOCUS

PM2-TN0123-300800-001-g12 TN0123 Homo sapiens cDNA, mRNA sequence.
BF377686
VERSION
KEYWORDS
SOURCE
ORGANISM

BF377686.1 GI:11339711
Homo sapiens (human)

REFERENCE
AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-TN0123-

300800-001-g12&t3=2000-08-30&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 11

High quality sequence stop: 329.

FEATURES

source

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/dev_stage="Adult"

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/notes="Organ: testis normal; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 56.5%; Score 32.2; DB 2; Length 329;

Best Local Similarity 50.9%; Pred. No. 4.6e+02;

Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGNNNNUGGCAUGCCUUGCGGCAUGGCUAAGG 53

DB 70 GTGACAGCTTCTTGAGAGCTCCATGGGCATGGCTATGGCATGGCTAAGG 122

RESULT 5

BF995707

LOCUS

PM1-GN0066-051100-002-c02 GN0066 Homo sapiens cDNA, mRNA sequence.

DEFINITION

BF995707

ACCESSION

BF995707

VERSION

BF995707.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 391)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM1&t2=PM1-GN0066-

051100-002-c02&t3=2000-11-05&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 23

High quality sequence stop: 243.

FEATURES

source

1. 391

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="GN0066"

/notes="Organ: placenta normal; Vector: puc18; Site 1:

SmaI; Site 2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

ORIGIN

Query Match 56.5%; Score 32.2; DB 4; Length 391;

Best Local Similarity 50.9%; Pred. No. 4.6e+02;

Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGNNNNUGGCAUGCCUUGCGGCAUGGCUAAGG 53

DB 147 GTGACAGCTTCTTGAGAGCTCCATGGGCATGGCTATGGCATGGCTAAGG 199

RESULT 6

AA134752/c

LOCUS

z119a11.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone

IMAGE:502364 5', mRNA sequence.

DEFINITION

AA134752

ACCESSION

AA134752

VERSION

AA134752.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 474)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,

Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.

and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

97044478

PUBMED

889549

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estowat@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1417 Std Error: 0.00

```

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 232.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3807352"
/db_xref="taxon:9606"
/clone="IMAGE:502364"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares pregnant uterus NBHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site: 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
ACTGGAGAAATCGCGCCGCTTTTITTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN
Query Match 56.5%; Score 32.2; DB 1; Length 474;
Best Local Similarity 50.9%; Pred. No. 4.8e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACUCCUCCGCGGNNNNNUGGCAUGCCUCCGCGCAUGGCUAAGG 53
DB 98 GTGACAGCTTCCTTGAGAAAGCTCCATGGCATGGCTATGGCGCTAAAG 46

RESULT 7
AU128462/c
LOCUS AU128462 NT2RP2 Homo sapiens cDNA clone NT2RP2003508 5', mRNA
sequence.
ACCESSION AU128462
VERSION AU128462.1 GI:10988816
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2003508"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="Vector: pMR18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 232.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
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/db_xref="GDB:3807352"
/db_xref="taxon:9606"
/clone="IMAGE:502364"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares pregnant uterus NBHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site: 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
ACTGGAGAAATCGCGCCGCTTTTITTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN
Query Match 56.5%; Score 32.2; DB 1; Length 474;
Best Local Similarity 50.9%; Pred. No. 4.8e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACUCCUCCGCGGNNNNNUGGCAUGCCUCCGCGCAUGGCUAAGG 53
DB 98 GTGACAGCTTCCTTGAGAAAGCTCCATGGCATGGCTATGGCGCTAAAG 46

RESULT 7
AU128462/c
LOCUS AU128462 NT2RP2 Homo sapiens cDNA clone NT2RP2003508 5', mRNA
sequence.
ACCESSION AU128462
VERSION AU128462.1 GI:10988816
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2003508"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="Vector: pMR18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 56.5%; Score 32.2; DB 1; Length 474;
Best Local Similarity 50.9%; Pred. No. 4.8e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACUCCUCCGCGGNNNNNUGGCAUGCCUCCGCGCAUGGCUAAGG 53
DB 98 GTGACAGCTTCCTTGAGAAAGCTCCATGGCATGGCTATGGCGCTAAAG 46

RESULT 7
AU128462/c
LOCUS AU128462 NT2RP2 Homo sapiens cDNA clone NT2RP2003508 5', mRNA
sequence.
ACCESSION AU128462
VERSION AU128462.1 GI:10988816
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2003508"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="Vector: pMR18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 56.5%; Score 32.2; DB 1; Length 474;
Best Local Similarity 50.9%; Pred. No. 4.8e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACUCCUCCGCGGNNNNNUGGCAUGCCUCCGCGCAUGGCUAAGG 53
DB 98 GTGACAGCTTCCTTGAGAAAGCTCCATGGCATGGCTATGGCGCTAAAG 46

RESULT 7
AU128462/c
LOCUS AU128462 NT2RP2 Homo sapiens cDNA clone NT2RP2003508 5', mRNA
sequence.
ACCESSION AU128462
VERSION AU128462.1 GI:10988816
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2003508"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="Vector: pMR18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 56.5%; Score 32.2; DB 1; Length 474;
Best Local Similarity 50.9%; Pred. No. 4.8e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACUCCUCCGCGGNNNNNUGGCAUGCCUCCGCGCAUGGCUAAGG 53
DB 98 GTGACAGCTTCCTTGAGAAAGCTCCATGGCATGGCTATGGCGCTAAAG 46

RESULT 7
AU128462/c
LOCUS AU128462 NT2RP2 Homo sapiens cDNA clone NT2RP2003508 5', mRNA
sequence.
ACCESSION AU128462
VERSION AU128462.1 GI:10988816
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2003508"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="Vector: pMR18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 56.5%; Score 32.2; DB 1; Length 474;
Best Local Similarity 50.9%; Pred. No. 4.8e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACUCCUCCGCGGNNNNNUGGCAUGCCUCCGCGCAUGGCUAAGG 53
DB 98 GTGACAGCTTCCTTGAGAAAGCTCCATGGCATGGCTATGGCGCTAAAG 46

RESULT 7
AU128462/c
LOCUS AU128462 NT2RP2 Homo sapiens cDNA clone NT2RP2003508 5', mRNA
sequence.
ACCESSION AU128462
VERSION AU128462.1 GI:10
```



```

RESULT 11
BP222743/c
LOCUS      583 bp    mRNA    linear    EST 15-SEP-2004
DEFINITION      Sugano cDNA library, COL0679 Homo sapiens cDNA clone
ACCESSION      BP222743
VERSION        COR04310, mRNA sequence.
KEYWORDS       BP222743.1 GI:52095648
SOURCE         EST.
ORGANISM       Homo sapiens (human)
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                Suzuki.Y., Yamashita.R., Shirotoma.M., Sakakibara.Y., Chiba.J.,
                Mizushima-Sugano.J., Nakai.K. and Sugano.S.
TITLE          Sequence comparison of human and mouse genes reveals a homologous
JOURNAL        block structure in the promoter regions
COMMENT        Genome Res. 14 (9), 1711-1718 (2004)
                Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
                     1..583
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="COR04310"
                        /cell_line="COL0679"
                        /clone_lib="Sugano cDNA library, COL0679"
                        /note="melanoma"
ORIGIN
Query Match      56.5%; Score 32.2; DB 5; Length 583;
Best Local Similarity 50.9%; Pred. No. 4.9e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY      1   GGGUCCACCUCGCGGUNNNNGGCCAUGCCTTCGATGGCATGCTAAAGG 53
           |||:|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      489 GTGACGACTTCTTGAGAAGCTCCATGGGCATGGCTATGGGCATGAAGG 437

RESULT 12
CB123548/c
LOCUS      635 bp    mRNA    linear    EST 29-JAN-2003
DEFINITION      K-EST0171939 L8SCKO Homo sapiens cDNA clone L8SCKO-33-H12 5', mRNA
ACCESSION      CB123548
VERSION        CB123548
KEYWORDS       CB123548.1 GI:28083069
SOURCE         EST.
ORGANISM       Homo sapiens (human)
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
                Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,U.M., Park,H.S., Kim,S. and
                Kim,Y.S.
TITLE          21C Frontier Korean EST Project 2001
JOURNAL        Unpublished (2002)
COMMENT        Contact: Kim YS
                Genome Research Center
                Korea Research Institute of Bioscience & Biotechnology
                52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                Tel : +82-42-860-4470
                Fax : +82-42-860-4409
                Email: yongsung@mail.kribb.re.kr
                Plate: 33 row: H column: 12
                High quality sequence stop: 635.
FEATURES             Location/Qualifiers

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source
1. .635
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="L8SCK0-33-H12"
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/cell_line="SCK"
/lab_host="Top10F"
/clone_lib="L8SCK0"
/notes="Organ: Liver; Vector: pTT3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN
Query Match 56.5%; Score 32.2; DB 6; Length 635;
Best Local Similarity 50.9%; Pred. No. 4.9e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGNNNNNUGGCAUGCCUCCUGGCGGAUGGCUAAGG 53
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 198 GTGACAGCTTCCTTGAGAGCTCCATGGCGCATGGCTATGGCGCTAAGG 146

RESULT 13
CK001771/c
LOCUS
DEFINITION
AGENCOURT 16379429 NIH_MGC_227 Homo sapiens cDNA clone
IMAGE:30717981 5', mRNA sequence.
CK001771
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 639)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Professor Miklas Palkovits
cDNA Library Preparation: Michael Brownstein / Ted Usdin
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM260 row: h column: 22
High quality sequence stop: 497.
Location/Qualifiers
1. .639
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30717981"
/tissue_type="Bulk tissue from Human Spinal cord"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 227"
/notes="Organ: brain/CNS; Vector: pDNR-LIB; Site 1: SfiI
(directional); Site 2: SfiI (directional); Library is
oligo-dT primed and directionally cloned.5' and 3'
adaptors were used in cloning as follows:
5'-AGCAGTGGTATCAACGAGTGCGCATACGCCGGG-3'
5'-ATTCTAGAGCGCGCGCATG-d(T)30N-IN-3. Full-length
enriched library was constructed using the Clontech

source
1. .667
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3827962"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 58"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCATG-dT(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

FEATURES
source
1. .667
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3827962"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 58"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCATG-dT(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN
Query Match 56.5%; Score 32.2; DB 2; Length 667;
Best Local Similarity 50.9%; Pred. No. 5e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGNNNNNUGGCAUGCCUCCUGGCGGAUGGCUAAGG 53
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 268 GTGACAGCTTCCTTGAGAGCTCCATGGCGCATGGCTATGGCGCTAAGG 216

RESULT 15
```

```
ORIGIN
Query Match 56.5%; Score 32.2; DB 7; Length 639;
Best Local Similarity 50.9%; Pred. No. 4.9e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGNNNNNUGGCAUGCCUCCUGGCGGAUGGCUAAGG 53
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 437 GTGACAGCTTCCTTGAGAGCTCCATGGCGCATGGCTATGGCGCTAAGG 385

RESULT 14
BF031657/c
LOCUS
DEFINITION
601558148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827962 5',
mRNA sequence.
BF031657
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 667)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM497 row: p column: 11
High quality sequence stop: 635.
Location/Qualifiers
1. .667
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3827962"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 58"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCATG-dT(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

FEATURES
source
1. .667
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3827962"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 58"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCATG-dT(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN
Query Match 56.5%; Score 32.2; DB 2; Length 667;
Best Local Similarity 50.9%; Pred. No. 5e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGNNNNNUGGCAUGCCUCCUGGCGGAUGGCUAAGG 53
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 268 GTGACAGCTTCCTTGAGAGCTCCATGGCGCATGGCTATGGCGCTAAGG 216

RESULT 15
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source
1. .635
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L8SCK0-33-H12"
/sex="M"
/cell_line="SCK"
/lab_host="Top10F"
/clone_lib="L8SCK0"
/notes="Organ: Liver; Vector: pTT3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN
Query Match 56.5%; Score 32.2; DB 6; Length 635;
Best Local Similarity 50.9%; Pred. No. 4.9e+02;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCUGCGGNNNNNUGGCAUGCCUCCUGGCGGAUGGCUAAGG 53
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 198 GTGACAGCTTCCTTGAGAGCTCCATGGCGCATGGCTATGGCGCTAAGG 146

RESULT 13
CK001771/c
LOCUS
DEFINITION
AGENCOURT 16379429 NIH_MGC_227 Homo sapiens cDNA clone
IMAGE:30717981 5', mRNA sequence.
CK001771
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 639)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Professor Miklas Palkovits
cDNA Library Preparation: Michael Brownstein / Ted Usdin
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM260 row: h column: 22
High quality sequence stop: 497.
Location/Qualifiers
1. .639
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30717981"
/tissue_type="Bulk tissue from Human Spinal cord"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 227"
/notes="Organ: brain/CNS; Vector: pDNR-LIB; Site 1: SfiI
(directional); Site 2: SfiI (directional); Library is
oligo-dT primed and directionally cloned.5' and 3'
adaptors were used in cloning as follows:
5'-AGCAGTGGTATCAACGAGTGCGCATACGCCGGG-3'
5'-ATTCTAGAGCGCGCGCATG-d(T)30N-IN-3. Full-length
enriched library was constructed using the Clontech
```

Job time : 2483.25 secs

BU657400/c
 LOCUS BU657400 671 bp mRNA linear EST 30-SEP-2002
 DEFINITION cl23902.z1 Hembase; Erythroid Precursor Cells (LCB:cl library) Homo
 sapiens cDNA clone cl23902 5', mRNA sequence.
 ACCESSION BU657400
 VERSION BU657400.1 GI:23369582
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 671)
 Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
 TITLE Gene Expression in Human Erythroid Precursor Cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jm7f@nih.gov
 The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
 Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
 analyses by National Institutes of Health Intramural Sequencing
 Center (NISC). More information available at:
 http://hembase.nidk.nih.gov
 Plate: 23 row: 9 column: 02
 Seq primer: 5' lambda-Triplex2 Sequencing Primer.

FEATURES
source

1..671
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="cl23902"
 /sex="unknown"
 /tissue_type="blood"
 /cell_type="Erythroid Precursor Cells"
 /cell_line="Primary Culture of Peripheral Blood
 Mononuclear Cells"
 /dev_stage="Precursor erythroblasts; GPA+ "
 /lab_host="DH5alpha"
 /clone_lib="Hembase; Erythroid Precursor Cells (LCB:cl
 library)"
 /notes="Organ: blood; Vector: pTriplex2; Site 1: SfiI;
 Site 2: SfiI; A complementary DNA (cDNA) library from
 human erythroid precursor cells was constructed using
 SMART PCR (polymerase chain reaction) cDNA Library
 Construction Kit (Clontech, Palo Alto, CA) according to
 the manufacturer's directions, but with slight
 modifications. Briefly, reverse transcription was
 performed in the presence of 1 umol/l peptide nucleic acid
 (PNA) oligos
 (N-terminal)-biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and
 (N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal)
 . Synthesized cDNA was digested with SfiI and
 size-selected on a 1% agarose gel (>800bp). Large-scale
 sequencing of the library was performed by the NIH
 Intramural Sequencing Center (NISC;
 Http://www.nisc.nih.gov/)."

ORIGIN

Query Match 56.5%; Score 32.2; DB 5; Length 671;
 Best Local Similarity 50.9%; Pred. No. 5e+02;
 Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
 QY 1 GGGUCCACCUCCGCGGUNNNNNUGGCAUGCCUUCGGGCAUGGCUAAGG 53
 Db 618 GTGACAGCTTCCTTGAGAGCTCCATGGCGATGGCTATGGCATGGCTAAGG 566

Search completed: March 15, 2005, 15:20:19

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 01:00:51 ; Search time 110.702 Seconds
(without alignments)
1069.494 Million cell updates/sec

Title: us-09-699-667E-66
Perfect score: 20
Sequence: 1 bkgcauggcuaggagacc 20
Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.4	92.0	20	AAZ57640	Aaz57640 Nucleotid
2	18.4	92.0	57	AAZ57636	Aaz57636 Trans-act
3	18.4	92.0	57	AAZ57638	Aaz57638 Trans-act
4	18.4	92.0	57	AAZ57637	Aaz57637 Trans-act
5	16.8	84.0	396	AAH30335	Aah30335 Human col
6	16.8	84.0	98146	ABD33150	Abd33150 Human can
7	15.8	79.0	772	AAH36243	Aah36243 Human mus
8	15.8	79.0	772	ABX59231	Abx59231 cDNA enco
9	15.8	79.0	772	ADJ29981	Adj29981 Human mus
10	15.8	79.0	11715	AAH81564	Aah81564 Genomic s
11	15.8	79.0	11724	AAH70102	Aah70102 Complete
12	15.8	79.0	11724	AAH57497	Aah57497 Human liv
13	15.8	79.0	11725	AAH57496	Aah57496 Human liv
14	15.8	79.0	11725	AAH79723	Aah79723 Human pro
15	15.8	79.0	11725	AAH32179	Aah32179 Human pro
16	15.8	79.0	11725	AAH54051	Aah54051 Human pro
17	15.8	79.0	13870	AAH56352	Aah56352 Human pro
18	15.6	78.0	98686	ADI80019	Adi80019 Human tra
19	15.6	78.0	348101	ADQ97146	Adq97146 Human can
20	15.4	77.0	353	ABX43915	Abx43915 Bovine ES

C 21	15.4	77.0	454	4	AA111117	AA11117 Probe #10
C 22	15.4	77.0	454	4	ABA52776	Abas2776 Human foe
C 23	15.4	77.0	454	4	AAI32382	Aai32382 Probe #10
C 24	15.4	77.0	454	4	ABA42350	Abas2350 Human bre
C 25	15.4	77.0	454	4	ABA22561	Abas22561 Probe #10
C 26	15.4	77.0	454	4	AAK26487	Aak26487 Human bon
C 27	15.4	77.0	454	4	AAK01029	Aak01029 Human bra
C 28	15.4	77.0	454	4	ABS26079	Abbs26079 Human liv
C 29	15.4	77.0	454	5	AAI01035	Aai01035 Probe #10
C 30	15.4	77.0	454	6	ABS01077	Abso1077 Human gen
C 31	15.4	77.0	1781	3	AAC69636	Aac69636 Human sec
C 32	15.4	77.0	3595	6	ABX84081	Abx84081 Human CDN
C 33	15.4	77.0	3595	12	ADN04534	Adn04534 Antipsoi
C 34	15.4	77.0	3595	12	ADQ97740	Adq97740 Human can
C 35	15.4	77.0	3595	13	ADQ84509	Adq84509 Human tum
C 36	15.4	77.0	3595	13	ACN39420	Acn39420 Tumour-as
C 37	15.4	77.0	3648	12	ADQ97744	Adq97744 Human can
C 38	15.4	77.0	20188	12	ADN33950	Adn33950 Human CDN
C 39	15.4	77.0	20190	10	ADC71539	Adc71539 Human NOV
C 40	15.4	77.0	41197	12	ADQ97739	Adq97739 Human can
C 41	15.4	77.0	57130	8	ABQ77243	Abq77243 Human MAR
C 42	15.4	77.0	135005	12	ADQ19501	Aad19501 Human sof
C 43	15.2	76.0	215	3	AAC13372	Aac13372 Human sec
C 44	15.2	76.0	273	12	ADQ20522	Adq20522 Human sof
C 45	15.2	76.0	434	4	AAK81439	Aak81439 Human imm

ALIGNMENTS

RESULT 1
AAZ57640
ID AAZ57640 standard; RNA; 20 BP.
XX
AC AAZ57640;
XX
DT 05-APR-2000 (first entry)
XX
DE Nucleotide sequence of bimolecular ribozyme RzB fragment.
XX
KW Bimolecular ribozyme; viral RNA cleavage; RzA fragment;
KW inherited disease; SS.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..8
FT /tag= a
FT /bound_moiety= "Bimolecular ribozyme RzB fragment"
FT /note= "Forms double-stranded region with bases 37-30 of
FT sequence AAZ57639"
FT misc_binding 15..20
FT /tag= b
FT /bound_moiety= "Bimolecular ribozyme RzB fragment"
FT /note= "Forms double-stranded region with bases 6-1 of
FT sequence AAZ57639"

WO9955856-A2.

04-NOV-1999.

29-APR-1999; 99WO-CA000391.

29-APR-1998; 98CA-02230203.

(UYSH) UNIV SHERBROOKE.

Perreault J, Ananvoranich S, Lafontaine D;

WPI; 2000-096791/08.

New construction of nucleic acid enzyme useful for biotechnological,
diagnostic and therapeutic applications.

```

XX
PS Example 5; Fig 4; 52pp; English.
CC This is the nucleotide sequence of binolecular ribozyme RzB fragment.
CC This ribozyme cleaves substrate SP1.1 (see AAZ57641). The invention
CC relates to a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed
CC to have a substrate binding portion with the following sequence 3'-UNNKN
CC -5'. The substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The
CC binding portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3'
CC to the cleavage site of the substrate. (cleavage site is represented by
CC *). At least one nucleotide is present 5' to the cleavage site of the
CC substrate sequence. The enzyme of the invention is used to cleave a
CC substrate nucleotide sequence at a specific cleavage site by mixing the
CC substrate with the enzyme. The enzyme is used to cleave viral RNA or RNA
CC causing for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
SQ Sequence 20 BP; 4 A; 6 C; 8 G; 0 T; 2 U; 0 Other;
      Query Match          92.0%; Score 18.4; DB 3; Length 20;
      Best Local Similarity 85.0%; Pred. No. 6.9;
      Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20
   :::|||||
Db 1 GCGCAUGGCUAAGGACCC 20

RESULT 2
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
AC AAZ57636;
XX
DT 05-APR-2000 (first entry)
DE Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzP1.1; ss.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound_moiety= "SP1.1 substrate (AAZ57641) bases 5-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX
PN WO955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT

```

```

PT diagnostic and therapeutic applications.
XX
PS Example 1; Fig 1A; 52pp; English.
XX
CC This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
CC cleaves substrate SP1.1 (see AAZ57641). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNKN-5'. The
CC substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
      Query Match          92.0%; Score 18.4; DB 3; Length 57;
      Best Local Similarity 85.0%; Pred. No. 7.7;
      Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20
   :::|||||
Db 38 UUCGCAUGGCUAAGGACCC 57

RESULT 3
AAZ57638
ID AAZ57638 standard; RNA; 57 BP.
XX
AC AAZ57638;
XX
DT 15-SEP-2003 (revised)
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; ss.
XX
OS Hepatitis D virus.
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound_moiety= "SP1.1 substrate bases (AAZ57641) 5-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX
XX WO955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX
XX WPI; 2000-096791/08.
XX

```

```

XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
XX Example 1; Fig 2; 52pp; English.
XX
CC This is the nucleotide sequence of a trans-acting antigenomic delta
CC ribozyme of the invention. This ribozyme cleaves substrate SPI.1 (see
CC AA257641). The invention relates to a nucleic acid enzyme (e.g.
CC deltaRzPl.1) that is constructed to have a substrate binding portion with
CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
CC sequence 5'-H'-GNNHNN-3'. The binding portion of the enzyme (ribozyme)
CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
CC (cleavage site is represented by *). At least one nucleotide is present
CC 5' to the cleavage site of the substrate sequence. The enzyme of the
CC invention is used to cleave a substrate nucleotide sequence at a specific
CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
CC to cleave viral RNA or RNA causing for example an inherited disease. The
CC enzymes also have other therapeutic, biotechnological and diagnostic
CC applications. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
Query Match 92.0%; Score 18.4; DB 3; Length 57;
Best Local Similarity 85.0%; Pred. No. 7.7;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGACCC 20
DB 38 CGGGCAUGGCUAAGGACCC 57
RESULT 4
AA257637
ID AA257637 standard; RNA; 57 BP.
XX
AC AA257637;
XX
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme, deltaRzPl.2 nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzPl.2; ss.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT misc_binding 1..6
FT /*tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /*tag= b
FT misc_binding 20..25
FT /*tag= c
FT /bound_moiety= "SPI.2 substrate bases (AA257634) 6-11"
FT stem_loop 30..45
FT /*tag= d
FT misc_binding 52..57
FT /*tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX
XX WO9955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;

```

```

XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
XX Example 1; Page; 52pp; English.
XX
CC This is the nucleotide sequence of ribozyme deltaRzPl.2. This ribozyme
CC cleaves substrate SPI.2 (see AA257634). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzPl.2) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'-GNNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications. Note: This
CC sequence is not shown in the specification, but has been derived from the
CC deltaRzPl.1 sequence (AA257636) shown in figure 1
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
Query Match 92.0%; Score 18.4; DB 3; Length 57;
Best Local Similarity 85.0%; Pred. No. 7.7;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGACCC 20
DB 38 UUCGCAUGGCUAAGGACCC 57
RESULT 5
AAH30335
ID AAH30335 standard; cDNA; 396 BP.
XX
AC AAH30335;
XX
DT 27-JUL-2001 (first entry)
XX
DE Human colon cancer cell line Km12L4-A cDNA library derived sequence #269.
XX
KW Human; diagnosis; colon cancer; cancer; malignant; chromosome mapping;
KW detection; colon cancer cell line Km12L4-A; ss.
XX
OS Homo sapiens.
XX
XX WO200018916-A2.
XX
XX 06-APR-2000.
XX
XX 23-SEP-1999; 99WO-US022226.
XX
XX 28-SEP-1998; 98US-0102161P.
XX
XX 28-SEP-1998; 98US-0102180P.
XX
XX 29-SEP-1998; 98US-0102380P.
XX
XX 28-OCT-1998; 98US-0103815P.
XX
XX 27-OCT-1998; 98US-0105877P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Williams LT, Escobedo J, Inniss WA, Garcia PD, Sudduth-Klinger J;
XX Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
XX Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
XX Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
XX WPI; 2000-293155/25.
XX
XX Polynucleotide library comprising 1079 defined sequences, useful in the

```

PT form of an array to detect cancer or susceptibility to cancer.

PS Claim 1; Page 262; 502pp; English.

XX The present invention describes a library of polynucleotides comprising
CC 1079 nucleotide sequences (given in AAH30067 to AAH31145). Also described
CC are: (1) an isolated polynucleotide (I) having at least 90% identity to
CC one of the 1079 sequences; (2) a recombinant host cell containing (I);
CC (3) an isolated polypeptide (II) encoded by (I); (4) an antibody that
CC specifically binds to (II); (5) a vector comprising (I); and (6) a method
CC of detecting differentially expressed genes correlated with a cancerous
CC state of a mammalian cell comprising detecting a gene product encoded by
CC 65 of the 1079 sequences given in the specification. The polynucleotides
CC are used to monitor patients having (or susceptible) to cancer to detect
CC potentially malignant events at a molecular level before they are
CC detectable at a gross morphological level. The polynucleotides are also
CC useful for monitoring the efficacy of various therapies and preventive
CC interventions. Polynucleotide probes based on the disclosed sequences are
CC useful for chromosome mapping and detection of transcription levels. The
CC 1079 polynucleotide sequences were derived from a human colon cancer cell
CC line Kml2L4-A cDNA library

XX SQ Sequence 396 BP; 130 A; 41 C; 104 G; 119 T; 0 U; 2 Other;

Query Match 84.0%; Score 16.8; DB 3; Length 396;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20

Db 23 CTGGCATGGCTAAGGACAC 42

RESULT 6

ABD33150

ID ABD33150 standard; DNA; 98146 BP.

XX AC ABD33150;

DT 18-NOV-2004 (first entry)

XX DE Human cancer-associated (CA) gene HD07-019.

XX KW Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
XX ds; cancer; cytostatic.

XX OS Homo sapiens.

XX PN WO2004058146-A2.

XX PD 15-JUL-2004.

XX PF 15-DEC-2003; 2003WO-US040081.

XX PR 17-DEC-2002; 2002US-00322281.

XX PA (SAGR-) SAGRES DISCOVERY INC.

XX PI Morris DW, Malandro MS;

XX DR WPI; 2004-499109/47.

XX PT Novel human cancer associated protein encoded within open reading frame
XX of cancer associated gene, useful as targets for diagnosing cancer.

XX PS Claim 16; SEQ ID NO 126; 182pp; English.

XX CC The invention relates to cancer-associated proteins (CAP) and the cancer-
XX associated (CA) nucleic acids encoding them. The invention also relates
XX to a method for treating cancers involving administering to a patient an
XX inhibitor of CAP, and a method of screening for anticancer activity in a
XX potential drug involving providing a cell that expresses a CA gene,
XX contacting a tissue sample derived from a cancer cell with an anticancer

CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 98146 BP; 28916 A; 17044 C; 18301 G; 33831 T; 0 U; 54 Other;

Query Match 84.0%; Score 16.8; DB 13; Length 98146;

Best Local Similarity 70.0%; Pred. No. 1.2e+02;

Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACCC 20

Db 46153 CTGGCATGGCTAAGGACAC 46172

RESULT 7

AAL36243/c

ID AAL36243 standard; DNA; 772 BP.

XX AC AAL36243;

DT 08-JAN-2002 (first entry)

XX DE Human musculoskeletal system related polynucleotide SEQ ID NO 2608.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
XX vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein;
XX musculoskeletal system; ds.

XX OS Homo sapiens.

XX PN WO200155367-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US0011338.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 07-JUL-2000; 2000US-0216880P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 11-JUL-2000; 2000US-0217496P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225266P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

XX PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226379P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
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PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-451937/48.
XX Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis.
XX Example 2; SEQ ID NO 2608; 781pp + Sequence Listing; English.
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 772 BP; 200 A; 179 C; 202 G; 191 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 772;
Best Local Similarity 68.4%; Pred. No. 2.5e+02;

QY 1 BKSGCAUGGCUAAGGACC 19
D5 :::|||:|||||
Db 84 TTGGCATGCTAAGGCTCC 66

RESULT 9
ADJ29981/c
ID ADJ29981 standard; DNA; 772 BP.
XX
AC ADJ29981;
XX
XX 20-MAY-2004 (first entry)
DT
XX
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2608.
XX
XX musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
KW gene therapy; vaccine; human; ds.
KW
XX Homo sapiens.
OS
XX US2004009488-A1.
PN
XX 15-JAN-2004.
PD
XX
PF 13-SEP-2002; 2002US-00242515.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 12-SEP-2000; 2000US-0232081P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
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PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
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PR 13-OCT-2000; 2000US-0239933P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
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PR 17-NOV-2000; 2000US-0249213P.
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PR 17-NOV-2000; 2000US-0249299P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2004-090458/09.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX
XX Disclosure; SEQ ID NO 2608; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytostatic and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated genomic DNA of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC <http://seqdata.uspto.gov/sequence.html?DocID=20040009488>.
XX
XX Sequence 772 BP; 200 A; 179 C; 202 G; 191 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 12; Length 772;
Best Local Similarity 68.4%; Pred. NO. 2.5e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGACC 19
Db 84 TTGGCATGGCTAAGGTCC 66
RESULT 10
ID AAN81564/c
XX AAN81564 standard; DNA; 11715 BP.
XX AAN81564;
XX 25-MAR-2003 (revised)
DT 05-DEC-1990 (first entry)
XX Genomic sequence encoding protein C.
XX Human protein C; blood coagulation disorders; ss.
XX Homo sapiens.
XX Location/Qualifiers
FH 2131..2200
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FT /label= exon I
FT 3464..3630
FT exon

FT /*tag= b
FT /label= exon II
FT 5093..5117
FT /*tag= c
FT /label= exon III
FT 5212..5349
FT /*tag= d
FT /label= exon IV
FT 5452..5586
FT /*tag= e
FT /label= exon VI
FT 8255..8397
FT /*tag= f
FT /label= exon VII
FT 9270..9387
FT /*tag= g
FT /label= exon VIII
FT 10517..12006
FT /*tag= h
FT /label= exon IX
XX
XX EP266190-A.
XX
XX 04-MAY-1988.
XX
XX 28-OCT-1987; 87EP-00309528.
XX
XX 29-OCT-1986; 86US-00924462.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Foster DC, Murray MJ, Berkner KL;
XX WPI; 1988-121259/18.
XX P-PSDB; AAP81205.
XX
XX Protein C DNA coding sequence and expression vector for prodn. - used for
PT treating blood coagulation disorders.
XX
XX Disclosure; Page ?; 35pp; English.
XX
XX In the construction of the full length protein C gene this sequence the
CC introns removed then is joined to a cDNA clone. The desired genomic:cDNA
CC is then generated by looping out of unwanted sequences using
CC oligonucleotide-directed deletion mutagenesis. The protein produced upon
CC transformation of mammalian host cells, contg. the recombinant DNA, has
CC substantially the same biological activity as natural protein C and is
CC hence useful in the treatment of blood coagulation disorders. See also
CC AAN81563. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 11715 BP; 2443 A; 3292 C; 3375 G; 2605 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 1; Length 11715;
Best Local Similarity 73.7%; Pred. NO. 3.3e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGACC 19
Db 877 GGCGCATGGCAAGGACC 859
RESULT 11
ID AAN70102/c
XX AAN70102 standard; DNA; 11724 BP.
XX
XX AAN70102;
XX
XX 25-MAR-2003 (revised)
DT 10-MAY-1991 (first entry)
XX
XX Complete genomic sequence of human Protein C.
XX Human Protein C; anti-coagulant; thrombosis; serine protease; ss.
KW

XX OS Homo sapiens.
XX PH Key
XX FT exon Location/Qualifiers
XX FT 2131..2200
XX FT /tag= a
XX FT /number= 1
XX FT /notes= "encodes amino acids -42 to -20"
XX FT 2201..3463
XX FT /tag= b
XX FT /number= 1
XX FT 2464..3630
XX FT /tag= c
XX FT /number= 2
XX FT /notes= "encodes amino acids -19 to +37"
XX FT 3631..5092
XX FT /tag= d
XX FT /number= 2
XX FT 5093..5117
XX FT /tag= e
XX FT /number= 3
XX FT /notes= "encodes amino acids 38 to 45"
XX FT 5118..5209
XX FT /tag= f
XX FT /number= 3
XX FT 5210..5347
XX FT /tag= g
XX FT /number= 4
XX FT /notes= "encodes amino acids 46 to 91"
XX FT 5348..5449
XX FT /tag= h
XX FT /number= 4
XX FT 5450..5584
XX FT /tag= i
XX FT /number= 5
XX FT /notes= "encodes amino acids 92 to 136"
XX FT 5585..8252
XX FT /tag= j
XX FT /number= 5
XX FT 8253..8395
XX FT /tag= k
XX FT /number= 6
XX FT /notes= "encodes amino acids 137 to 184"
XX FT 8396..9267
XX FT /tag= l
XX FT /number= 6
XX FT 9268..9385
XX FT /tag= m
XX FT /number= 7
XX FT /notes= "encodes amino acids 185 to 223"
XX FT 9386..10514
XX FT /tag= n
XX FT /number= 7
XX FT 10515..11104
XX FT /tag= o
XX FT /number= 8
XX FT /notes= "encodes amino acids 224 to 419"
XX FT 11151..11156
XX FT /tag= q
XX FT 11173
XX FT /tag= r
XX FT polyA_signal
XX FT 11380..11385
XX FT /tag= s
XX FT 11399
XX FT /tag= t
XX FT
XX PN EP215548-A.
XX PD 25-MAR-1987.
XX PP 26-JUN-1986;
XX PR 27-JUN-1985;
86EP-00304970.
85US-00749600.

PR 15-AUG-1985; 85US-00766109.
XX (ZYMO) ZYMOGENETICS INC.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Murray MJ, Berkner KL, Foister DC, Davie EW;
XX WPI; 1987-081505/12.
DR P-PSDB; AAP70855.
XX Human protein C or activated protein C - prepd. using expression vector
XX capable of integration in mammalian host cell DNA.
PS Claim 2; Page 33; 52pp; English.
XX A lambda gt cDNA library was prepared from human liver mRNA. The library
CC was screened with iodine-125 labelled antibody to human protein C. A cDNA
CC which lacked the coding sequence for the pre-pro peptide and the forat 23
CC amino acids of protein C was isolated and used as a hybridisation probe.
CC The remainder of the coding sequence was obtained from a human genomic
CC DNA library in lambda Charon 4A. Recombinantly produced protein C can be
CC used to treat thrombotic disorders such as venous thrombosis. (Updated on
CC 25-MAR-2003 to correct PA field.)
XX Sequence 11724 BP; 2445 A; 3302 C; 3370 G; 2607 T; 0 U; 0 Other;
SQ Query Match 79.0%; Score 15.8; DB 1; Length 11724;
Best Local Similarity 73.7%; Pred. No. 3.3e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 BKSGCAUGGCUAAGGACC 19
DB 877 GCGCATGCGCAAGGACC 859
:::|||||
RESULT 12
AAH57497/c
ID AAH57497 standard; cDNA; 11724 BP.
XX
XX AAH57497;
XX DT 10-SEP-2001 (first entry)
XX Human liver cell specific cDNA sequence SEQ ID NO:337.
XX Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
XX liver; uterus; ovary; stomach; intestine; kidney; pancreas; sg;
XX metabolic disease; developmental disease; cytostatic; immunomodulatory;
XX neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX OS Homo sapiens.
XX WO200132927-A2.
XX 10-MAY-2001.
XX 02-NOV-2000; 2000WO-US030396.
XX 04-NOV-1999; 99US-0163508P.
XX (INCY-) INCYTE GENOMICS INC.
XX Sornasse T, Seilhamer JJ, Watson GA;
XX WPI; 2001-291057/30.
XX New cell and tissue specific polynucleotides useful for diagnosis,
XX prognosis or monitoring of treatments for disorders where the gene is
XX associated with a cancer, immunopathology or neuropathology.
PS Claim 1; Page 254-257; 327pp; English.
XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide

CC sequences (I). (I) can have cytostatic, immunomodulatory and
 CC neuroprotective activities, and can be used in gene therapy. (I) and
 CC proteins (II) encoded by then are used in high throughput screening
 CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
 CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
 CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
 CC agents. Expression of (I) in a sample indicates the differentiation of
 CC embryonic stem cells into a tissue selected from brain, heart, kidney,
 CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
 CC to produce an expression profile that defines a metabolic or
 CC developmental process, treatment, condition, disease or disorder. The
 CC gene profile can be used for diagnosis, prognosis or monitoring of
 CC treatments and for investigating a predisposition to a disorder where the
 CC gene is associated with a cancer, immunopathology or neuropathology
 XX

SQ Sequence 11724 BP; 2443 A; 3298 C; 3375 G; 2608 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 4; Length 11724;

Best Local Similarity 73.7%; Pred. No. 3.3e+02;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19

DB 877 GCGCATGGCAAGGACC 859

RESULT 13

AAT32796/c

ID AAT32796 standard; DNA; 11725 BP.

XX AC AAT32796;

XX DT 25-MAR-2003 (revised)

XX DT 05-NOV-1996 (first entry)

XX DE Human protein C gene.

XX KW Activated protein C; serine protease; thrombosis; thrombolytic;
 KW fibrinolytic; antithrombotic; blood clotting; therapy; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 1. -2250

XX FT /tag= a

XX FT /codon_start= 2131. .2133

XX FT 2251. .3463

XX FT /tag= b

XX FT 3464. .3630

XX FT /tag= c

XX FT 3631. .5092

XX FT /tag= d

XX FT 5093. .5117

XX FT /tag= e

XX FT 5118. .5209

XX FT /tag= f

XX FT 5210. .5347

XX FT /tag= g

XX FT 5348. .5449

XX FT /tag= h

XX FT 5450. .5583

XX FT /tag= i

XX FT 5583. .8252

XX FT /tag= j

XX FT 8253. .8395

XX FT /tag= k

XX FT 8395. .9268

XX FT /tag= l

XX FT misc_difference 9268

XX FT /tag= m

XX FT /note= "base 9268 is given as 'y' in the specification"

XX FT 9269. .9386

XX FT /tag= n

FT intron 9387. .10515

FT /tag= o

FT exon 10516. .11725

FT /tag= p

FT polyA_signal 11152. .11157

FT /tag= q

FT polyA_signal 11381. .11386

FT /tag= r

XX US5516650-A.

XX PD 14-MAY-1996.

XX PF 08-APR-1994;

XX 94US-00225253.

XX PR 27-JUN-1985;

XX PR 85US-00749600.

XX PR 29-OCT-1986;

XX PR 86US-00924462.

XX PR 08-DEC-1987;

XX PR 87US-00130370.

XX PR 28-FEB-1989;

XX PR 89US-00317205.

XX PR 10-SEP-1990;

XX PR 90US-00582131.

XX PR 04-DEC-1992;

XX PR 92US-00987532.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Murray MJ, Berkner KL, Foster DC;

XX DR WPI, 1996-251006/25.

XX DR P-PSDB; AAW02600.

XX PT New DNA encoding modified forms of opt. activated protein C - and related

XX PT transformed cells for prodn. of recombinant protein C for use e.g. as an

XX PT anti-thrombotic agent.

XX PS Example 1; Fig 4A-D; 34pp; English.

XX CC A genomic DNA fragment (AAT32796) codes for human full-length protein C

XX CC (AAW02600), a zymogen of a serine protease that plays an important role

XX CC in blood clotting and in the generation of fibrinolytic activity in vivo.

XX CC It was obtd. from a human genomic library in phage Charon 4A using a

XX CC partial cDNA clone as probe. A complete cDNA clone (AAT32795) was also

XX CC produced. Protein C-encoding nucleic acids can be used for large-scale

XX CC prodn. of protein C, or variants modified to improve cleavage between the

XX CC heavy and light chains of the circulating intermediate. (Updated on 25-

XX CC MAR-2003 to correct PF field.)

XX SQ Sequence 11725 BP; 2444 A; 3295 C; 3372 G; 2613 T; 0 U; 1 Other;

Query Match 79.0%; Score 15.8; DB 2; Length 11725;

Best Local Similarity 73.7%; Pred. No. 3.3e+02;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19

DB 877 GCGCATGGCAAGGACC 859

RESULT 14

AAT32796/c

ID AAT32796 standard; DNA; 11725 BP.

XX AC AAT32796;

XX DT 11-DEC-1997 (first entry)

XX DE Human protein C gene.

XX KW Protein C; transgenic animal; sheep; rabbit; cattle; goat; milk;

XX KW blood clotting; anticoagulant; human; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 3520. .3630

FT intron /*tag= a
 FT 3631..5092
 FT /*tag= b
 FT 5093..5117
 FT /*tag= c
 FT 5118..5209
 FT /*tag= d
 FT 5210..5347
 FT /*tag= e
 FT 5348..5449
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 FT 5450..5584
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 FT 8253..8395
 FT /*tag= i
 FT 8396..9268
 FT /*tag= j
 FT 9269..9386
 FT /*tag= k
 FT 9387..10515
 FT /*tag= l
 FT 10516..11102
 FT /*tag= m

PN WO9720043-A1.

XX 05-JUN-1997.

XX 26-NOV-1996; 96WO-US018866.

XX 30-NOV-1995; 95US-00565074.

PR 13-JUN-1996; 96US-0019692P.

XX (ZYMO) ZYMOGENETICS INC.

PA (PPLT-) PPL THERAPEUTICS.

PI Garner I, Cottingham I, Temperley SM, Foster DC, Sprecher CA;

PI Prunkard DB;

XX WPI; 1997-310599/28.

DR P-PSDB; AAW25086.

XX Production of protein C in transgenic animal - useful for high quantity protein C production with therapeutic value.

PS Claim 6; Page 49-58; 99pp; English.

XX This DNA sequence comprises human genomic DNA encoding protein C (AAW25086). A claimed method for producing human protein C in the milk of a transgenic animal involves: (a) providing a DNA construct comprising a transgenic animal signal and a protein C propeptide, operably linked to DNA encoding two chain cleavage site-modified protein C, the 2 DNA sequences being linked to elements required for protein C expression in a mammary gland of a host female animal, esp. the beta-lactoglobulin gene promoter (see AAT79725); and (b) using the DNA construct to breed a transgenic animal (esp. sheep, rabbit, cattle, goat) that produces protein C in its milk, at least 90% of the protein C being in the two-chain form. Modification of the protein C two-chain cleavage site (see AAW25085) improves the maturation of recombinant protein C from single chain to two-chain form. Also claimed is a non-human mammalian embryo containing in its nucleus a heterologous DNA segment encoding cleavage site-modified protein C

XX Sequence 11725 BP; 2444 A; 3298 C; 3375 G; 2608 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 2; Length 11725;

Best Local Similarity 73.7%; Pred. No. 3.3e+02;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19

:::|||||

Db 877 GGCGCATGGCAAGGACC 859

RESULT 15

AAZ32179/c

ID AAZ32179 standard; cDNA; 11725 BP.

XX AAZ32179;

XX 13-JAN-2000 (first entry)

XX Human protein C nucleotide sequence.

XX Human; coding sequence polymorphism; vascular pathology gene;

KW polymorphic site; phenotype correlation; forensic; paternity testing;

KW medicine; genetic analysis; vascular disease; da.

OS Homo sapiens.

XX WO9950454-A2.

PN 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006473.

XX 01-APR-1998; 98US-00054272.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

PI Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;

XX WPI; 1999-620066/53.

DR P-PSDB; AAY49560.

XX Determination of polymorphisms in genes, especially those identifying predisposition to vascular disease.

PS Claim 1; Fig 23; 134pp; English.

XX AAZ32159 to AAZ32194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise polymorphic sites as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the CC polymorphic site is different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic analysis. CC AAY49550 to AAY49573 represent the proteins which correspond to some of the reference alleles

XX Sequence 11725 BP; 2444 A; 3298 C; 3375 G; 2608 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 2; Length 11725;

Best Local Similarity 73.7%; Pred. No. 3.3e+02;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19

:::|||||

Db 877 GGCGCATGGCAAGGACC 859

Search completed: March 15, 2005, 11:20:24

Job time : 114.702 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 01:00:51 ; Search time 315.5 Seconds
(without alignments)
1069.494 Million cell updates/sec

Title: US-09-699-667E-62

Perfect score: 57

Sequence: 1 ggguccaccuccgcggun.....cgggcaugcuaagggacc 57

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	57	3	Aaz57638 Trans-act
2	47.4	83.2	57	3	Aaz57636 Trans-act
3	47.4	83.2	57	3	Aaz57637 Trans-act
4	34	59.6	37	3	Aaz57639 Nucleotid
5	32.2	56.5	267	2	Aav88169 EST clone
6	32.2	56.5	1404	6	Abss1814 Human mdd
7	32.2	56.5	1430	6	Aah33539 Human col
8	32.2	56.5	1430	6	Ab190291 Human pol
9	32.2	56.5	1878	4	Aai60621 Human pol
10	32.2	56.5	1927	4	Aai58835 Human pol
11	32.2	56.5	1927	5	Adq99056 DNA encod
12	32.2	56.5	1927	9	Adb48816 Novel hum
13	32.2	56.5	2206	4	Abk43595 DNA encod
14	32.2	56.5	2206	12	Adi53982 cDNA enco
15	32.2	56.5	2258	4	Aah16046 Human cDN
16	32.2	56.5	2404	4	Aah15794 Human cDN
17	32.2	56.5	2519	2	Aav54124 Human mem
18	32.2	56.5	2700	4	Aas21257 Human cDN
19	32.2	56.5	2700	8	ACA03616 cDNA enco
20	32.2	56.5	2700	8	ABx89154 DNA encod

c 21	32.2	56.5	2700	8	ACD41808	Accl41808 Human sec
c 22	32.2	56.5	2700	8	ACA04037	Aca04037 Human cDN
c 23	32.2	56.5	2700	9	ADA45546	Ada45546 Novel hum
c 24	32.2	56.5	2700	9	ADA75977	Ada75977 Human PRO
c 25	32.2	56.5	2700	9	ADA18627	Ada18627 Human PRO
c 26	32.2	56.5	2700	9	ADA61250	Ada61250 Homo sapi
c 27	32.2	56.5	2700	9	ADB19035	ADB19035 Novel hum
c 28	32.2	56.5	2700	9	ADB27576	ADB27576 cDNA enco
c 29	32.2	56.5	2700	9	ADA86055	Ada86055 Novel hum
c 30	32.2	56.5	2700	9	ADB15619	ADB15619 Human PRO
c 31	32.2	56.5	2700	9	ADA47405	Ada47405 Human PRO
c 32	32.2	56.5	2700	9	ADA67200	Ada67200 Human PRO
c 33	32.2	56.5	2700	9	ADB30207	ADB30207 cDNA enco
c 34	32.2	56.5	2700	9	ADA85503	Ada85503 Novel hum
c 35	32.2	56.5	2700	9	ADA96715	Ada96715 Human PRO
c 36	32.2	56.5	2700	9	ADA79019	Ada79019 Human PRO
c 37	32.2	56.5	2700	9	ADA87158	Ada87158 Novel hum
c 38	32.2	56.5	2700	9	ADB16360	ADB16360 Human PRO
c 39	32.2	56.5	2700	9	ADA91452	Ada91452 Novel hum
c 40	32.2	56.5	2700	9	ADB14515	ADB14515 Human PRO
c 41	32.2	56.5	2700	9	ADB18476	ADB18476 Novel hum
c 42	32.2	56.5	2700	9	ADA93691	Ada93691 Human PRO
c 43	32.2	56.5	2700	9	ADB19587	ADB19587 Novel hum
c 44	32.2	56.5	2700	9	ADB12899	ADB12899 Human PRO
c 45	32.2	56.5	2700	9	ACD98437	ACD98437 Novel hum

ALIGNMENTS

RESULT 1
AAZ57638
ID AAZ57638 standard; RNA; 57 BP.
XX
AC AAZ57638;
DT 15-SEP-2003 (revised)
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; ss.
XX
OS Hepatitis D virus.
XX
PH Key
FT misc_binding Location/Qualifiers
FT 1..6 /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19 /tag= b
FT /tag= c
FT misc_binding 20..25 /tag= d
FT /tag= e
FT stem_loop 30..45 /tag= f
FT /tag= g
FT misc_binding 52..57 /tag= h
FT /tag= i
FT /note= "Forms a double stranded region with bases 6-11"
XX
WO9955856-A2.
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-CA000391.
XX
PR 29-APR-1996; 98CA-02230203.
XX
PA (UYSH) UNIV SHERBROOKE.
XX
PI Perreault J, Ananvoranich S, Lafontaine D;
XX

```
DR WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
XX Example 1; Fig 2; 52pp; English.
XX
XX This is the nucleotide sequence of a trans-acting antigenomic delta
CC ribozyme of the invention. This ribozyme cleaves substrate SPI.1 (see
CC AAZ57641). The invention relates to a nucleic acid enzyme (e.g.
CC deltaRzPl.1) that is constructed to have a substrate binding portion with
CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
CC sequence 5'-H'*GNHNN-3'. The binding portion of the enzyme (ribozyme)
CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
CC (cleavage site is represented by *). At least one nucleotide is present
CC 5' to the cleavage site of the substrate sequence. The enzyme of the
CC invention is used to cleave a substrate nucleotide sequence at a specific
CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
CC to cleave viral RNA or RNA causing for example an inherited disease. The
CC enzymes also have other therapeutic, biotechnological and diagnostic
CC applications. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
SQ
Query Match 100.0%; Score 57; DB 3; Length 57;
Best Local Similarity 89.5%; Pred. No. 2.9e-07;
Matches 51; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUGCCUUCGGCAUGCUAAGGGACCC 57
Db 1 GGGUCCACCUCCUGCGGCGCGACCGUGGCAUGCCUUCGGCAUGCUAAGGGACCC 57
RESULT 2
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
XX
XX AAZ57636;
XX
XX 05-APR-2000 (first entry)
XX
XX Trans-acting antigenomic delta ribozyme, deltaRzPl.1 nucleotide sequence.
DE
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzPl.1; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound_moiety= "SPI.1 substrate (AAZ57641) bases 5-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX
XX WO9955856-A2.
PN
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
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PI Perreault J, Ananvoranich S, Lafontaine D;
XX
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
XX Example 1; Fig 1A; 52pp; English.
XX
XX This is the nucleotide sequence of ribozyme deltaRzPl.1. This ribozyme
CC cleaves substrate SPI.1 (see AAZ57641). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzPl.1) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'*GNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
XX Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
SQ
Query Match 83.2%; Score 47.4; DB 3; Length 57;
Best Local Similarity 78.9%; Pred. No. 0.00032;
Matches 45; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCCUGCGGNNNNNUGGCAUGCCUUCGGCAUGCUAAGGGACCC 57
Db 1 GGGUCCACCUCCUGCGGCGCGACCGUGGCAUGCCUUCGGCAUGCUAAGGGACCC 57
RESULT 3
AAZ57637
ID AAZ57637 standard; RNA; 57 BP.
XX
XX AAZ57637;
XX
XX 05-APR-2000 (first entry)
XX
XX Trans-acting antigenomic delta ribozyme, deltaRzPl.2 nucleotide sequence.
DE
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzPl.2; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound_moiety= "SPI.2 substrate bases (AAZ57634) 6-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX
XX WO9955856-A2.
PN
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
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XX PI Perreault J, Ananvoranich S, Lafontaine D;
XX DR WPI; 2000-096791/08.
XX PR New construction of nucleic acid enzyme useful for biotechnological,
XX PT diagnostic and therapeutic applications.
XX PA Example 1; Page; 52pp; English.
XX CC This is the nucleotide sequence of ribozyme deltaRzP1.2. This ribozyme
XX CC cleaves substrate SP1.2 (see AA257634). The invention relates to a
XX CC nucleic acid enzyme (e.g. deltaRzP1.2) that is constructed to have a
XX CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
XX CC substrate of the enzyme has the sequence 5'-H'*GNHNN-3'. The binding
XX CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
XX CC cleavage site of the substrate (cleavage site is represented by *). At
XX CC least one nucleotide is present 5' to the cleavage site of the substrate
XX CC sequence. The enzyme of the invention is used to cleave a substrate
XX CC nucleotide sequence at a specific cleavage site by mixing the substrate
XX CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
XX CC for example an inherited disease. The enzymes also have other
XX CC therapeutic, biotechnological and diagnostic applications. Note: This
XX CC sequence is not shown in the specification, but has been derived from the
XX CC deltaRzP1.1 sequence (AA257636) shown in figure 1
XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match 83.2%; Score 47.4; DB 3; Length 57;
Best Local Similarity 78.9%; Pred. No. 0.00032;
Matches 45; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCAUGCCUUCGGCGAUGGCUAAGGGACCC 57
DB 1 GGGUCCACCUCCGCGGNNNNNUGGCAUGCCUUCGGCGAUGGCUAAGGGACCC 57

RESULT 4
AAZ57639
ID AAZ57639 standard; RNA; 37 BP.
XX AC AAZ57639;
XX DT 05-APR-2000 (first entry)
XX DE Nucleotide sequence of bimolecular ribozyme RZA fragment.
XX KW Bimolecular ribozyme; viral RNA cleavage; RZA fragment;
XX KW inherited disease; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_binding 1..6
XX FT /tag= a
XX FT /bound moiety= "RzB fragment of bimolecular ribozyme"
XX FT /note= "Forms double-stranded region with bases 20-16 of
XX FT sequence AAZ57640"
XX FT stem_loop 7..19
XX FT /tag= b
XX FT /bound moiety= "Ribozyme substrate p1.1"
XX FT /tag= c
XX FT /bound moiety= "Forms double-stranded region with bases 11-6 of
XX FT sequence AAZ57641"
XX FT /tag= d
XX FT /bound moiety= "RzB fragment of bimolecular ribozyme"
XX FT /note= "Forms double-stranded region with bases 8-1 of
XX FT sequence AAZ57640"
XX PN WO955856-A2.
XX
```

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PD 04-NOV-1999.
XX PF 29-APR-1999; 99WO-CA000391.
XX PR 29-APR-1998; 98CA-02230203.
XX PA (UYSH ) UNIV SHERBROOKE.
XX PI Perreault J, Ananvoranich S, Lafontaine D;
XX DR WPI; 2000-096791/08.
XX PT New construction of nucleic acid enzyme useful for biotechnological,
XX PT diagnostic and therapeutic applications.
XX PA Example 5; Fig 4; 52pp; English.
XX CC This is the nucleotide sequence bimolecular ribozyme RZA fragment. This
XX CC ribozyme cleaves substrate SP1.1 (see AA257641). The invention relates to
XX CC a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
XX CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
XX CC substrate of the enzyme has the sequence 5'-H'*GNHNN-3'. The binding
XX CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
XX CC cleavage site of the substrate (cleavage site is represented by *). At
XX CC least one nucleotide is present 5' to the cleavage site of the substrate
XX CC sequence. The enzyme of the invention is used to cleave a substrate
XX CC nucleotide sequence at a specific cleavage site by mixing the substrate
XX CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
XX CC for example an inherited disease. The enzymes also have other
XX CC therapeutic, biotechnological and diagnostic applications
XX SQ Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;

Query Match 59.6%; Score 34; DB 3; Length 37;
Best Local Similarity 82.4%; Pred. No. 5;
Matches 28; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCGCGGNNNNNUGGCGAUGC 34
DB 1 GGGUCCACCUCCGCGGNNNNNUGGCGAUGC 34

RESULT 5
AAV88169/c
ID AAV88169 standard; cDNA; 267 BP.
XX AC AAV88169;
XX DT 12-FEB-1999 (first entry)
XX DE EST clone DT470.
XX KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
XX KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
XX KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
XX KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX OS Homo sapiens.
XX PN WO9845437-A2.
XX PD 15-OCT-1998.
XX PF 10-APR-1998; 98WO-US006956.
XX PR 10-APR-1997; 97US-00837312.
XX PA (GEMY ) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
XX PI Spaulding V, Agostino MJ;
XX DR WPI; 1999-070078/06.
```


CC proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene therapy
 CC and vaccine production. N and P may be used in the prevention, diagnosis
 CC and treatment of diseases associated with inappropriate P expression. For
 CC example, N and P may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of P by expressing inactive proteins or to
 CC supplement the patients own production of P. Additionally, N may be used
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAH77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922

XX SQ Sequence 1430 BP; 494 A; 227 C; 260 G; 446 T; 0 U; 3 Other;

Query Match 56.5%; Score 32.2; DB 4; Length 1430;
 Best Local Similarity 50.9%; Pred. No. 49;
 Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACUCCUCCGCGGNNNNNNUGGCGAUGCCUCCGCGCAUGGCUAAGG 53
 DB 98 GTGRCAGCTTCTTGAGAGCTCCATGGCGCATGGCTATGGCGCTAAAGG 46

RESULT 8

ABU90291/c
 ID ABL90291 standard; cDNA; 1430 BP.

XX AC ABL90291;

XX DT 24-MAY-2002 (first entry)

XX DE Human polynucleotide SEQ ID NO 853.

XX KW Cytostatic; immunosuppressive; nontropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.

XX OS Homo sapiens.

XX PN WO200190304-A2.

XX PD 29-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016450.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX DR WPI; 2002-122018/16.

XX DR P-PSDB; ABB89882.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.

XX PS Claim 4; SEQ ID NO 853; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL9449-ABL90853) and proteins
 CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences

XX SQ Sequence 1430 BP; 494 A; 227 C; 260 G; 446 T; 0 U; 3 Other;

Query Match 56.5%; Score 32.2; DB 6; Length 1430;
 Best Local Similarity 50.9%; Pred. No. 49;
 Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACUCCUCCGCGGNNNNNNUGGCGAUGCCUCCGCGCAUGGCUAAGG 53
 DB 98 GTGRCAGCTTCTTGAGAGCTCCATGGCGCATGGCTATGGCGCTAAAGG 46

RESULT 9

AAI60621/c
 ID AAI60621 standard; cDNA; 1878 BP.

XX AC AAI60621;

XX DT 22-OCT-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 4610.

XX KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662191.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX DR P-PSDB; AAM41465.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

XX PS Claim 1; SEQ ID NO 4610; 10078pp; English.

CC given in the specification, its translated or protein coding portion, its
 CC extracellular portion or its active domain. The GPCR-like polypeptides
 CC and polynucleotides are useful for the treatment of diseases of
 CC ophthalmic, neurological, immunological and nephritic systems. They may
 CC also be used to treat hormonal dysfunction, cancer, atherosclerosis and
 CC diabetes. The antibodies are useful for detecting or quantitating the
 CC polypeptide in tissue. The polypeptides can also be used as molecular
 CC weight markers and as a food supplement. This sequence represents a human
 CC polynucleotide of the invention.

SQ Sequence 1927 BP; 615 A; 327 C; 367 G; 618 T; 0 U; 0 Other;

Query Match 56.5%; Score 32.2; DB 5; Length 1927;

Best Local Similarity 50.9%; Pred. No. 53;

Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNNUGGCAUGCCUUGCGGCAUGGCUAAGG 53
 DB 594 GTGACAGCTTCCTTGAGAGCTCCATGGCATGCTATGGCATGGCTAAAGG 542

RESULT 12

ADB48816/c
 ID ADB48816 standard; cDNA; 1927 BP.

XX ADB48816;

XX 04-DEC-2003 (first entry)

XX Novel human cDNA SEQ ID NO 726.

XX ss; cancer; neurodegenerative disease; human.

XX Homo sapiens.

XX US2003104529-A1.

XX 05-JUN-2003.

XX 04-JAN-2002; 2002US-00037270.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 19-JUL-2000; 2000US-00620312.

XX (ZHOU/) ZHOU P.

XX (TANG/) TANG Y T.

XX (LIUC/) LIU C.

XX (ASUN/) ASUNDI V.

XX (DRMA/) DRMANAC R T.

XX Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;

XX WPI; 2003-678194/64.

XX New polynucleotide, useful for treating diseases e.g., cancer or

XX neurodegenerative diseases.

XX Claim 1; SEQ ID NO 726; 99pp; English.

XX The invention relates to a polynucleotide comprising a sequence given in
 CC the specification, or its mature protein-coding portion, or its
 CC complement. The polynucleotide is useful for treating diseases e.g.,
 CC cancer or neurodegenerative diseases and many others listed in the
 CC specification. The present sequence represents a novel human cDNA. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=20030104529.

XX Sequence 1927 BP; 615 A; 327 C; 367 G; 618 T; 0 U; 0 Other;

Query Match

Best Local Similarity 56.5%; Score 32.2; DB 9; Length 1927;

Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGNNNNNNUGGCAUGCCUUGCGGCAUGGCUAAGG 53
 DB 594 GTGACAGCTTCCTTGAGAGCTCCATGGCATGCTATGGCATGGCTAAAGG 542

RESULT 13
 ADB43595/c
 ID ADB43595 standard; cDNA; 2206 BP.

XX ADB43595;

XX 05-JUN-2002 (first entry)

XX DNA encoding novel central nervous system protein #175.

XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy; gene; ss.

XX Homo sapiens.

XX WO200155318-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001332.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 28-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 14-AUG-2000; 2000US-0225758P.

XX 14-AUG-2000; 2000US-0225759P.

XX 18-AUG-2000; 2000US-0226279P.

XX 22-AUG-2000; 2000US-0226681P.

XX 22-AUG-2000; 2000US-0226868P.

XX 23-AUG-2000; 2000US-0227182P.

XX 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 06-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 08-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0231968P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-581633/65.
DR P-PSDB; AAU87265.
XX
PT New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
PT
XX Claim 1; SEQ ID NO 185; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiotensin, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 56.5%; Score 32.2; DB 4; Length 2206;
Best Local Similarity 50.9%; Pred. No. 55;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
QY 1 GGGUCCACUCCUGCGGUNNNUGGCGAUGCCUUCGGCAUGGCUAAGG 53
DB 884 GTGACAGCTTCTTGAGAGCTCCATGGCATGGCTATGGCATGGCTAAGG 832

RESULT 14
ADI53982/c
ID ADI53982 standard; cDNA; 2206 BP.
XX AC ADI53982;
XX AC
XX DT 22-APR-2004 (first entry)
XX XX
XX cDNA encoding novel human protein seq id 185.
XX
XX neuroprotective; neurotropic; antiparkinsonian; anticonvulsant;
KW antidiabetic; antirheumatic; antiarthritic; dermatological;
KW antiinflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;
KW anti-HIV; hepatotropic; virucide; antibacterial; fungicide;
KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
KW cardiovascular; antiarteriosclerotic; antiarrhythmic; cardiac;
KW nephrotropic; litholytic; cytostatic; gene therapy; neural disorder;
KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
KW amyotrophic lateral sclerosis; multiple sclerosis;
KW immune system disorder; diabetes; rheumatoid arthritis;
KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;
KW inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; infectious disease;
KW HIV infection; hepatitis infection; bacterial infection;
KW fungal infection; parasitic infection; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;
KW renal disorder; acute glomerulonephritis; pyelonephritis;
KW renal lithiasis; proliferative disorder; cancerous diseases; human; gene;
88.
XX
XX Homo sapiens.
XX
XX US2004018969-A1.
XX
XX 29-JAN-2004.
XX
XX 17-JAN-2001; 2001US-00764875.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
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PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
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PR 16-AUG-2000; 2000US-0226279P.
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PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
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PR 17-NOV-2000; 2000US-0249209P.

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PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251869P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2004-122079/12.
DR P-PSDB; ADI54580.
XX
XX New polypeptides and nucleic acid molecules, useful for detecting,
PT preventing, diagnosing, prognosticating, treating or ameliorating medical
PT conditions e.g. neural disorders, reproductive disorders or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 185; 413pp; English.
XX
XX The invention describes an isolated polypeptide comprising an amino acid
CC sequence at least 90% identical to: a polypeptide fragment, domain,
CC epitope, or full-length protein of any one of 607 amino acid sequences
CC (I) described in the specification; a polypeptide fragment of (I), or the
CC encoded sequence contained in (II), having biological activity; or a
CC variant, allelic variant, or a species homologue of (I). The polypeptides
CC and nucleic acid molecules are useful for detecting, preventing,
CC diagnosing, prognosticating, treating or ameliorating medical conditions
CC such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease,
CC Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,
CC
CC
Query Match 56.5%; Score 32.2; DB 12; Length 2206;
Best Local Similarity 50.9%; Pred. No. 55;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCCGGGNNNNNNNUGGCAUGCCUUCGGCGCAUGGCUAAGG 53
DB 884 GTGACAGCTTCTTGAGAGCTCCATGGGCGATGGCTATGGCGATGCTAAAGG 832
RESULT 15
AAH16046/c
ID AAH16046 standard; cDNA; 2258 BP.
XX
AC AAH16046;
XX
DT 26-JUN-2001 (first entry)
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XX Human cDNA sequence SEQ ID NO:14719.
DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
KW Homo sapiens.
OS
XX EP1074617-A2.
PN
XX 07-FEB-2001.
PD
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
DR
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
XX Claim 8; SEQ ID NO 14719; 2537pp + Sequence Listing; English.
PS
XX
XX The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dr primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 2258 BP; 608 A; 435 C; 473 G; 742 T; 0 U; 0 Other;
Query Match 56.5%; Score 32.2; DB 4; Length 2258;
Best Local Similarity 50.9%; Pred. No. 56;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCCGGGNNNNNNNUGGCAUGCCUUCGGCGCAUGGCUAAGG 53
DB 1458 GTGACAGCTTCTTGAGAGCTCCATGGGCGATGGCTATGGCGATGCTAAAGG 1406
Search completed: March 15, 2005, 11:20:13
Job time : 321.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:18:52 ; Search time 94.5 Seconds
(without alignments)
986.961 Million cell updates/sec

Title: US-09-699-667E-62

Perfect score: 57
Sequence: 1 ggguccaccucccggun.....cggggaugcuaaggagacc 57

Scoring table: IDENTITY NUCCDX

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/prodata1/ina/5B COMB.seq.*
- 3: /cgn2_6/prodata1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata1/ina/PCUS COMB.seq.*
- 6: /cgn2_6/prodata1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	32.2	56.5	2319	4	US-09-380-287A-9
C 3	30.2	53.0	13818	4	US-09-902-540-1102
C 4	30	52.6	1740	4	US-09-252-991A-6553
C 5	30	52.6	2469	4	US-09-252-991A-6519
C 6	29.6	51.9	80	1	US-08-238-963A-16
C 7	29.6	51.9	83	3	US-08-646-695-12
C 8	29.6	51.9	83	5	PCT-US96-06053-12
C 9	29.6	51.9	84	1	US-08-238-963A-13
C 10	29.6	51.9	84	1	US-08-238-963A-14
C 11	29.6	51.9	86	1	US-08-238-963A-6
C 12	29.6	51.9	2358	4	US-09-902-540-2667
C 13	29.6	51.9	13706	4	US-09-902-540-1124
C 14	29.6	51.9	14311	3	US-08-646-695-1
C 15	29.6	51.9	14311	3	US-08-646-695-7
C 16	29.6	51.9	14311	5	PCT-US96-06053-1
C 17	29.6	51.9	14311	5	PCT-US96-06053-7
C 18	29.4	51.6	52	1	US-08-741-881-40
C 19	29.4	51.6	52	1	US-08-741-881-80
C 20	29.4	51.6	52	1	US-08-739-158-40
C 21	29.4	51.6	52	1	US-08-739-158-80
C 22	29.4	51.6	52	2	US-08-739-167-40
C 23	29.4	51.6	52	2	US-08-739-167-80
C 24	29.4	51.6	52	3	US-08-404-796-40
C 25	29.4	51.6	52	3	US-08-404-796-80
C 26	29.4	51.6	52	3	US-08-331-869-40
C 27	29.4	51.6	52	3	US-08-331-869-80

ALIGNMENTS

RESULT 1

US-09-620-312D-726/c
; Sequence 726, Application US/09620312D
; Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aiding J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 726
LENGTH: 1927
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (88)..(1224)
US-09-620-312D-726

Query Match 56.5%; Score 32.2; DB 4; Length 1927;
Best Local Similarity 50.9%; Pred. No. 18;
Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GGGUCCACCUCGCGGUNNNNNUGGCGCAUGCCUCCGCGCAUGGCUAAGG 53

Db 594 GTGACAGCTTCCTTGAGAGCTCCATGGCATGGCTATGGCATGGCTAAGG 542

[illegible]


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US96-06053-12

Query Match          51.9%; Score 29.6; DB 5; Length 83;
Best Local Similarity 52.3%; Pred. No. 44;
Matches 23; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNUGGCAUGCCUUCGGGCAUGGC 47
Db 17 TCCACCTCTCGCGTCCGACCTGGGCATCCGAAGGAGGACGTC 60

RESULT 9
US-08-238-963A-13
; Sequence 13, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,963A
; FILING DATE: May 5, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/821,155
; FILING DATE: January 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The letter "N" stands for
; any base.
; US-08-238-963A-14

Query Match          51.9%; Score 29.6; DB 1; Length 84;
Best Local Similarity 65.9%; Pred. No. 44;
Matches 29; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNUGGCAUGCCUUCGGGCAUGGC 47
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RESULT 11
US-08-238-963A-6
; Sequence 6, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
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; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,963A
; FILING DATE: May 5, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/821,155
; FILING DATE: January 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The letter "N" stands for
; any base.
; US-08-238-963A-14

Query Match          51.9%; Score 29.6; DB 1; Length 84;
Best Local Similarity 65.9%; Pred. No. 44;
Matches 29; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNUGGCAUGCCUUCGGGCAUGGC 47
Db 18 UCCACUCCUCCGGGUTCCGACUCCUGGCAUCCGAAGGAGGACGUC 61

RESULT 11
US-08-238-963A-6
; Sequence 6, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
```

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,963A
FILING DATE: May 5, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/821,155
FILING DATE: January 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 207/093
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-238-963A-6

Query Match 51.9%; Score 29.6; DB 1; Length 86;
Best Local Similarity 65.9%; Pred. No. 45;
Matches 29; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNUGGCAUGCCUUGCGGCAUGC 47
DB 20 UCCACCUCCUGCGGNNNNNUGGCAUGCCUUGCGGCAUGC 63

RESULT 12
US-09-902-540-2667
Sequence 2667, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2667
LENGTH: 2358
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-2667

Query Match 51.9%; Score 29.6; DB 4; Length 2358;
Best Local Similarity 51.9%; Pred. No. 1.2e+02;
Matches 27; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 3 GUCCACCUCCUGCGGNNNNNUGGCAUGCCUUGCGGCAUGCUAAGGA 54
DB 1048 GTCCCCCACTTCACGACCTGTACGCGACGCTTCGAGCAGCGCTACGCGA 1099

RESULT 13
US-09-902-540-1124/c
Sequence 1124, Application US/09902540

Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1124
LENGTH: 13706
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1124

Query Match 51.9%; Score 29.6; DB 4; Length 13706;
Best Local Similarity 51.9%; Pred. No. 2.1e+02;
Matches 27; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 3 GUCCACCUCCUGCGGNNNNNUGGCAUGCCUUGCGGCAUGCUAAGGA 54
DB 6442 GTCCCCCACTTCACGACCTGTACGCGACGCTTCGAGCAGCGCTACGCGA 6391

RESULT 14
US-08-646-695-1
Sequence 1, Application US/08646695
Patent No. 6168943
GENERAL INFORMATION:
APPLICANT: Rose, John K.
TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,695
FILING DATE: On Even Date Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 760..2025
FEATURE:
NAME/KEY: CDS

Job time : 98.5 secs

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/ LOCATION: 2092..2886
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 2946..3632
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3774..5306
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 5429..11755
/ US-08-646-695-1

Query Match      51.9%; Score 29.6; DB 3; Length 14311;
Best Local Similarity 52.3%; Pred. No. 2.1e+02;
Matches 23; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY      4 UCCACCUCCUGCGGNNNNNUGGCGAUGCCUUCGGGCAUGGC 47
DB      11874 TCCACCTCTCGCGGTCCGACCTGGGCATCCGAAGGAGGACGTC 11917

RESULT 15
US-08-646-695-7/c
; Sequence 7, Application US/08646695
; Patent No. 6168943
; GENERAL INFORMATION:
; APPLICANT: Rose, John K.
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,695
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-646-695-7

Query Match      51.9%; Score 29.6; DB 3; Length 14311;
Best Local Similarity 52.3%; Pred. No. 2.1e+02;
Matches 23; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY      4 UCCACCUCCUGCGGNNNNNUGGCGAUGCCUUCGGGCAUGGC 47
DB      2438 TCCACCTCTCGCGGTCCGACCTGGGCATCCGAAGGAGGACGTC 2395
```

Search completed: March 15, 2005, 15:26:37

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 11:20:37 ; Search time 205.285 Seconds
(without alignments)
1066.957 Million cell updates/sec

Title: US-09-699-667E-63
Perfect score: 37
Sequence: 1 ggguccaccuccgcgggunnnnmgggcaugcgcc 37

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4316768

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	37	AAZ57639	Nucleotid
2	35.4	95.7	57	AAZ57636	Trans-act
3	35.4	95.7	57	AAZ57637	Trans-act
4	34	91.9	57	AAZ57638	Trans-act
5	30.4	82.2	48	ADR47040	Adr47040
6	30.4	82.2	48	ADT48965	Adt48965
7	30.4	82.2	51	AAQ86173	Primer HD
8	30.4	82.2	52	AAQ86204	Sindbis/H
9	30.4	82.2	52	AAT31151	HDV rever
10	30.4	82.2	52	AAT30817	HDV riboz
11	30.4	82.2	52	AAV42394	Nested PC
12	30.4	82.2	52	AAV42426	Forward P
13	30.4	82.2	52	AAV60154	Nested PC
14	30.4	82.2	52	AAV60185	Reverse P
15	30.4	82.2	52	AAV70746	Reverse P
16	30.4	82.2	52	AAV70714	Nested pr
17	30.4	82.2	52	AAZ92930	Hepatitis
18	30.4	82.2	52	AAZ92970	Hepatitis
19	30.4	82.2	52	AAZ92843	Hepatitis
20	30.4	82.2	52	AAZ92803	Hepatitis

21	30.4	82.2	52	6	AAZ38850	Alphaviru
22	30.4	82.2	52	6	AAZ38810	Alphaviru
23	30.4	82.2	52	6	ABK46276	HDV anti
24	30.4	82.2	52	6	ABK46316	Hepatitis
25	30.4	82.2	52	12	ADI30383	Hepatitis
26	30.4	82.2	52	12	ADI30423	Hepatitis
27	30.4	82.2	52	12	ADQ13982	Eukaryoti
28	30.4	82.2	52	12	ADQ13942	Eukaryoti
29	30.4	82.2	57	12	ADH10551	Hepatitis
30	29	78.4	56	2	AAZ59264	Nested pr
31	29	78.4	56	2	AAZ58506	Nested pr
32	29	78.4	56	8	ABX81463	Sindbis v
33	29	78.4	56	9	ADA50686	Sindbis v
34	28	75.7	45	2	AAZ78132	Hepatitis
35	24	64.9	52	2	AAQ46668	Substrate
C 36	23.4	63.2	57	12	ADP69915	LacZnlb12
C 37	23	62.2	36	3	AAA35618	Permutin
C 38	23	62.2	58	2	AAT38753	Primer us
C 39	23	62.2	58	5	AAZ28149	Primer #3
40	22.4	60.5	36	2	AAQ73470	Porcine i
41	22.4	60.5	39	2	AAQ58518	Sequence
C 42	22.2	60.0	60	6	ABN45577	Human spl
C 43	22.2	60.0	54	12	ADP75787	Mycobacte
C 44	22	59.5	33	7	ADI92828	Mutant Tt
45	22	59.5	33	7	ADI92829	Mutant Tt

ALIGNMENTS

RESULT 1	
AAZ57639	
ID AAZ57639 standard; RNA; 37 BP.	
AC AAZ57639;	
XX	
DT 05-APR-2000 (first entry)	
DE	Nucleotide sequence of bimolecular ribozyme RZA fragment.
XX	
KW Bimolecular ribozyme; viral RNA cleavage; RZA fragment;	
KW inherited disease; ss.	
XX	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT misc_binding	1. .6
FT	/tag= a
FT	/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT	/note= "Forms double-stranded region with bases 20-16 of sequence AAZ57640"
FT	7. .19
FT	/tag= b
FT	20. .25
FT	/tag= c
FT	/bound_moiety= "Ribozyme substrate Pl.1"
FT	/note= "Forms double-stranded region with bases 11-6 of sequence AAZ57641"
FT	30. .37
FT	/tag= d
FT	/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT	/note= "Forms double-stranded region with bases 8-1 of sequence AAZ57640"
XX	
PN WO955856-A2.	
XX	
PD 04-NOV-1999.	
XX	
PF 29-APR-1999;	99WO-CA000391.
XX	
PR 29-APR-1998;	98CA-02230203.
XX	
PA (UYSH) UNIV SHERBROOKE.	

```
XX
PI Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
DR
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
XX Example 5; Fig 4; 52pp; English.
PS
XX This is the nucleotide sequence bimolecular ribozyme R2A fragment. This
CC ribozyme cleaves substrate SPI.1 (see AAZ57641). The invention relates to
CC a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
XX Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;
SQ
Query Match 100.0%; Score 37; DB 3; Length 37;
Best Local Similarity 83.8%; Pred.No. 0.045; Indels 0; Gaps 0;
Matches 31; Conservative 6; Mismatches 0;
QY 1 GGGUCCACCUCCUGCGGNNNNNNNUGGCGAUGCGCC 37
Db 1 GGGUCCACCUCCUGCGGCGGCCGACCGGCGAUGCGCC 37
RESULT 2
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
XX
AC AAZ57636;
XX
XX 05-APR-2000 (first entry)
XX
XX Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
DE
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzP1.1; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound_moiety= "SPI.1 substrate (AAZ57641) bases 5-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-11"
XX
XX WO9955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
```

```
PA (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
DR
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
XX Example 1; Fig 1A; 52pp; English.
PS
XX This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
CC cleaves substrate SPI.1 (see AAZ57641). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
XX Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
SQ
Query Match 95.7%; Score 35.4; DB 3; Length 57;
Best Local Similarity 81.1%; Pred.No. 0.18; Indels 0; Gaps 0;
Matches 30; Conservative 6; Mismatches 1;
QY 1 GGGUCCACCUCCUGCGGNNNNNNNUGGCGAUGCGCC 37
Db 1 GGGUCCACCUCCUGCGGCGGCCGACCGGCGAUGCGCC 37
RESULT 3
AAZ57637
ID AAZ57637 standard; RNA; 57 BP.
XX
AC AAZ57637;
XX
XX 05-APR-2000 (first entry)
XX
XX Trans-acting antigenomic delta ribozyme, deltaRzP1.2 nucleotide sequence.
DE
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzP1.2; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound_moiety= "SPI.2 substrate bases (AAZ57634) 6-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-11"
XX
XX WO9955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
```

XX PA (UYSH) UNIV SHERBROOKE.
 XX PI Perreault J, Ananvoranich S, Lafontaine D;
 XX XX WPI; 2000-096791/08.
 XX DR
 XX PT New construction of nucleic acid enzyme useful for biotechnological,
 XX FT diagnostic and therapeutic applications.
 XX PS Example 1; Page; 52pp; English.
 XX CC This is the nucleotide sequence of ribozyme deltaRzPl.2. This ribozyme
 CC cleaves substrate Sp1.2 (see AA257634). The invention relates to a
 CC nucleic acid enzyme (e.g. deltaRzPl.2) that is constructed to have a
 CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
 CC substrate of the enzyme has the sequence 5'-H*GNNHNN-3'. The binding
 CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
 CC cleavage site of the substrate (cleavage site is represented by *). At
 CC least one nucleotide is present 5' to the cleavage site of the substrate
 CC sequence. The enzyme of the invention is used to cleave a substrate
 CC nucleotide sequence at a specific cleavage site by mixing the substrate
 CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
 CC for example an inherited disease. The enzymes also have other
 CC therapeutic, biotechnological and diagnostic applications. Note: This
 CC sequence is not shown in the specification, but has been derived from the
 CC deltaRzPl.1 sequence (AA257636) shown in figure 1
 XX
 XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
 Query Match 95.7%; Score 35.4; DB 3; Length 57;
 Best Local Similarity 81.1%; Pred. No. 0.18;
 Matches 30; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGUCCACCUCUCCGCGGUNNNNNNUGGCGCAUGC 37
 Db 1 GGGUCCACCUCUCCGCGGUCGCGGCGCAUGC 37
 RESULT 4
 AA257638
 ID AA257638 standard; RNA; 57 BP.
 XX
 XX AC AA257638;
 XX
 XX DT 15-SEP-2003 (revised)
 XX DT 05-APR-2000 (first entry)
 XX
 XX DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
 XX KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
 XX KW inherited disease; ss.
 XX OS Hepatitis D virus.
 XX
 XX FH Key Location/Qualifiers
 XX FT misc_binding 1..6
 XX FT /*tag= a
 XX FT /note= "Forms double stranded region with bases 52-57"
 XX FT
 XX FT stem_loop 7..19
 XX FT /*tag= b
 XX FT 20..25
 XX FT /*tag= c
 XX FT 30..45
 XX FT /bound_moiety= "Sp1.1 substrate bases (AA257641) 5-11"
 XX FT stem_loop
 XX FT 52..57
 XX FT /*tag= d
 XX FT 52..57
 XX FT /*tag= e
 XX FT /note= "Forms a double stranded region with bases 6-11"
 XX
 XX PN WO9955856-A2.
 XX PD 04-NOV-1999.

XX 29-APR-1999; 99WO-CA000391.
 XX PR 29-APR-1998; 98CA-02230203.
 XX PA (UYSH) UNIV SHERBROOKE.
 XX PI Perreault J, Ananvoranich S, Lafontaine D;
 XX XX WPI; 2000-096791/08.
 XX PT New construction of nucleic acid enzyme useful for biotechnological,
 XX FT diagnostic and therapeutic applications.
 XX PS Example 1; Fig 2; 52pp; English.
 XX CC This is the nucleotide sequence of a trans-acting antigenomic delta
 CC ribozyme of the invention. This ribozyme cleaves substrate Sp1.1 (see
 CC AA257641). The invention relates to a nucleic acid enzyme (e.g.
 CC deltaRzPl.1) that is constructed to have a substrate binding portion with
 CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
 CC sequence 5'-H*GNNHNN-3'. The binding portion of the enzyme (ribozyme)
 CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
 CC (cleavage site is represented by *). At least one nucleotide is present
 CC 5' to the cleavage site of the substrate sequence. The enzyme of the
 CC invention is used to cleave a substrate nucleotide sequence at a specific
 CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
 CC to cleave viral RNA or RNA causing for example an inherited disease. The
 CC enzymes also have other therapeutic, biotechnological and diagnostic
 CC applications. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
 Query Match 91.9%; Score 34; DB 3; Length 57;
 Best Local Similarity 82.4%; Pred. No. 0.57;
 Matches 28; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGUCCACCUCUCCGCGGUNNNNNNUGGCGCAUGC 34
 Db 1 GGGUCCACCUCUCCGCGGUCGCGGCGCAUGC 34
 RESULT 5
 AD47040
 ID AD47040 standard; DNA; 48 BP.
 XX
 XX AC AD47040;
 XX
 XX DT 18-NOV-2004 (first entry)
 XX
 XX DE Dengue virus vaccine oligonucleotide #15.
 XX KW ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
 XX KW prem protein; C protein; NS1 protein signal; vaccine; cervical cancer;
 XX KW viral disease; antigen; dendritic cell; immune response;
 XX KW human papillomavirus.
 XX OS Unidentified.
 XX
 XX PN WO2004072274-A1.
 XX
 XX PD 26-AUG-2004.
 XX
 XX PF 30-JAN-2004; 2004WO-CN000088.
 XX
 XX PR 30-JAN-2003; 2003CN-00115272.
 XX PR 30-JAN-2003; 2003CN-00115273.
 XX
 XX PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
 XX PA (TENG-) TENGGEN BIOMEDICAL CO.
 XX PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
 XX
 XX PI Pang X;

```

XX WPI; 2004-625870/60.
XX
XX Virus-like particle vaccines containing dengue virus recombinant replicon
PT as core for carrier, applicable in preventives or/and remedies for tumors
PT like cervical cancer and viral diseases.
XX
XX Example 4; SEQ ID NO 37; 38pp; Chinese.
XX
XX A dengue virus recombinant replicon has a deletion of the complete coding
CC sequence for preM protein of dengue virus and also includes elements of
CC e.g. the non-coding region in the whole of the 5'-end, the coding region
CC of the front 20 amino acids in the C protein, and the coding region of
CC NS1 protein signal; coding regions of all non-structural proteins. The
CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to an oligonucleotide used in the
CC recombinant replicon of the invention.
XX
XX Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
SQ

```

```

XX Query Match 82.2%; Score 30.4; DB 13; Length 48;
XX Best Local Similarity 59.4%; Pred. No. 11;
XX Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCCUGCGGNNNNNNNUGGCGAUGCG 35
DB 17 TCACCTCTCGCGTCCGACCTGGGCATCCG 48

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XX RESULT 7
XX AAQ86173 standard; DNA; 51 BP.
XX
XX AAQ86173;
AC
XX 25-MAR-2003 (revised)
DT 21-NOV-1995 (first entry)
XX
XX Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.
DE
XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
KW transcription initiation; non-structural protein; subgenomic fragment;
KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
KW primer; polymerase chain reaction; cystic fibrosis; ss.
XX
XX Synthetic.
OS
XX WO9507994-A2.
PN
XX 23-MAR-1995.
PD
XX
XX 15-SEP-1994; 94WO-US010469.
PF
XX
XX 15-SEP-1993; 93US-00122791.
PR
XX 18-FEB-1994; 94US-00198450.
PR
XX
XX (VIAG-) VIAGENE INC.
PA
XX
XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
XX
XX WPI; 1995-131362/17.
DR
XX
XX New alpha virus vectors for gene therapy - of viral infection, cancer,
XX auto-immune disease, etc., and as vaccines.
PT
XX
XX Example 2; Page 68; 260pp; English.
PS
XX
XX The sequences given in AAQ86167-81 are primers which were used in the
CC generation of plasmid DNA which initiates Sindbis infection. The
CC amplified DNA sequences were used in the construction of a eukaryotic
CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
CC comprise a 5' sequence capable of initiating transcription of an
CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
CC proteins, a viral junction region which has been inactivated such that
CC viral transcription of the subgenomic fragment is prevented, and an
CC alphavirus RNA polymerase recognition sequence. Inactivation of the viral

```

CC junction region prevents transcription of the subgenomic fragment making
 CC vectors such as this suitable for a wide variety of applications, eg.
 CC gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 82.2%; Score 30.4; DB 2; Length 51;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCUCCGCGGUNNNNNNUGGCGAUGCG 35
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 8
 AAQ86204
 ID AAQ86204 standard; DNA; 52 BP.

XX AC AAQ86204;

XX AC AAQ86204;

DT 25-MAR-2003 (revised)

DT 23-NOV-1995 (first entry)

XX DE Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.

XX KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcriptions initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.

XX OS Synthetic.

XX PN WO9507994-A2.

XX PD 23-MAR-1995.

XX PF 15-SEP-1994; 94WO-US010469.

XX PR 15-SEP-1993; 93US-00122791.

XX PR 18-FEB-1994; 94US-00198450.

XX PA (VIAG-) VIAGENE INC.

XX PI Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;

XX XX WPI; 1995-131362/17.

XX PT New alpha virus vectors for gene therapy - of viral infection, cancer,
 PT auto-immune disease, etc., and as vaccines.

XX PS Example 7; Page 114; 260pp; English.

XX CC The sequences given in AAQ86200-15 are primers which were used in the
 CC production of alphavirus vectors expressing multiple heterologous genes.
 CC These vectors are eukaryotic layered vector initiation systems (ELVIS)
 CC derived from Sindbis. ELVIS's comprise a 5' sequence capable of
 CC initiating transcription of an alphavirus, a nucleotide sequence encoding
 CC alphavirus non-structural proteins, a viral junction region which has
 CC been inactivated such that viral transcription of the subgenomic fragment
 CC is prevented, and an alphavirus RNA polymerase recognition sequence.
 CC Inactivation of the viral junction region prevents transcription of the
 CC subgenomic fragment making vectors such as this suitable for a wide
 CC variety of applications, eg. gene therapy for the treatment of cystic
 CC fibrosis. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 82.2%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCUCCGCGGUNNNNNNUGGCGAUGCG 35
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 9

AAAT31151

ID AAAT31151 standard; DNA; 52 BP.

XX AC AAAT31151;

XX DT 12-SEP-1996 (first entry)

XX DE HDV reverse primer HDV17-68.

XX KW Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
 KW polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;
 KW ribozyme; ss.

XX OS Synthetic.

XX PN WO9617072-A2.

XX PD 06-JUN-1996.

XX PF 30-NOV-1995; 95WO-US015490.

XX PR 30-NOV-1994; 94US-00348472.

XX PR 18-JAN-1995; 95US-00376184.

XX PR 15-MAR-1995; 95US-00405827.

XX PA (CHIR) CHIRON VIAGENE INC.

XX PI Dubensky TW, Polo JM, Ibanez CE, Chang SM, Jolly DJ, Driver DA;
 PI Belli BA;

XX DR WPI; 1996-277785/28.

XX PT New recombinant alpha-virus vectors - used to develop prods and methods
 PT for use in gene therapy and in the prodn. of vaccines.

XX PS Example 7; Page 120; 256pp; English.

XX CC Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)
 CC nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)
 CC for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV
 CC (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment
 CC contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping
 CC synthesis is used in a second round of PCR using primers HDV49-XC and
 CC SIN276-SPE. The resulting construct contains the expression cassette
 CC elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction
 CC region/Sindbis structural protein genes/Sindbis 3'-end untranslated
 CC region, designated p5-28s. This was inserted into pCDNA3. Packaging cell
 CC line cassettes were constructed that allow inducible expression of
 CC structural proteins via alphavirus vectors

XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 82.2%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCUCCGCGGUNNNNNNUGGCGAUGCG 35
 Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 10

AAT30817

ID AAT30817 standard; DNA; 52 BP.

XX AC AAT30817;

XX XX AAT30817;


```

PT recombinant alpha:virus particles.
XX Example 7; Col 103; 140pp; English.
XX PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC invention. The specification describes a DNA alphavirus structural
CC protein expression cassette which comprises an inducible promoter and an
CC alphavirus structural protein gene, where the promoter directs the
CC expression of the alphavirus structural protein gene upon induction of
CC the promoter within a cell, and where prior to induction within the cell,
CC the expression cassette does not express sufficient quantities of
CC structural proteins to be cytotoxic to a BHK cell containing the
CC expression cassette. The products may be used to inhibit pathogens and
XX CC stimulate an immune response
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match      82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 11;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUCGCGGCGGNNNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 13
AAV60154
ID AAV60154 standard; DNA; 52 BP.
XX AC AAV60154;
XX DT 25-MAR-2003 (revised)
DT 04-DEC-1998 (first entry)
XX DE Nested PCR primer HDV17-68.
XX KW Eukaryotic layered vector initiation system; stimulate; immune response;
KW Sindbis; PCR primer; ss.
XX OS Synthetic.
OS Hepatitis D virus.
XX PN US5814482-A.
XX PD 29-SEP-1998.
XX PF 30-OCT-1996; 96US-00739158.
XX PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 14-SEP-1994; 94WO-US010469.
PR 30-NOV-1994; 94US-00348472.
PR 18-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX (POLO/) POLO J M.
PA (DUBE/) DUBENSKY T W.
PA (JOLLY) JOLLY D J.
PA (DRIV/) DRIVER D A.
XX PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX WPI; 1998-541753/46.
XX Eukaryotic layered vector initiation system - containing eukaryotic
PT promoter and heterologous antigen coding sequence, useful for stimulating
PT immune response.
XX Example 3; Col 71-72; 144pp; English.
XX PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
CC ribozyme sequence. The product is used in the course of the invention.

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CC The specification describes an eukaryotic layered vector initiation
CC system, based on Sindbis. The eukaryotic layered vector initiation system
CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC infection by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match      82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 11;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUCGCGGCGGNNNNNNNUGGCGAUGC 35
   :||||:||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 14
AAV60185
ID AAV60185 standard; DNA; 52 BP.
XX AC AAV60185;
XX DT 25-MAR-2003 (revised)
DT 04-DEC-1998 (first entry)
XX DE Reverse PCR primer HDV17-68.
XX KW Eukaryotic layered vector initiation system; stimulate; immune response;
KW Sindbis; PCR primer; ss.
XX OS Synthetic.
XX PN US5814482-A.
XX PD 29-SEP-1998.
XX PF 30-OCT-1996; 96US-00739158.
XX PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 14-SEP-1994; 94WO-US010469.
PR 30-NOV-1994; 94US-00348472.
PR 18-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX (POLO/) POLO J M.
PA (DUBE/) DUBENSKY T W.
PA (JOLLY) JOLLY D J.
PA (DRIV/) DRIVER D A.
XX PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX WPI; 1998-541753/46.
XX Eukaryotic layered vector initiation system - containing eukaryotic
PT promoter and heterologous antigen coding sequence, useful for stimulating
PT immune response.
XX Example 5; Col 108; 144pp; English.
XX PCR primers AAV60184-85 are used in the course of the invention. The
CC specification describes an eukaryotic layered vector initiation system,
CC based on Sindbis. The eukaryotic layered vector initiation system
CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.

```

CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 11;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUCGCGGUNNNNNUGGCGAUGCG 35
:||||:||||:||||:||||:||||:||||: ||
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15

AAV70746
ID AAV70746 standard; DNA; 52 BP.

XX AC AAV70746;

XX 20-MAR-2003 (revised)

DT 02-FEB-1999 (first entry)

XX Reverse PCR primer HDV17-68 used to amplify Hepatitis delta virus.

XX Alphavirus vector construct; gene therapy; PCR primer; ss.

XX Synthetic.

OS Hepatitis D virus.

XX US5843723-A.

XX 01-DEC-1998.

XX 30-OCT-1996; 96US-00739167.

XX 15-SEP-1993; 93US-00122791.

PR 18-FEB-1994; 94US-00198450.

PR 20-NOV-1994; 94US-00348472.

PR 20-JAN-1995; 95US-00376184.

PR 15-MAR-1995; 95US-00404796.

XX (CHIR) CHIRON CORP.

XX Chang SMW, Jolly DJ, Dubensky TW, Belli BA, Ibanez CE, Driver DA;

PI Polo JM;

XX WPI; 1999-044581/04.

XX Alphavirus vectors constructs containing a 5' promoter of viral cDNA by
PT in vitro transcription - used in gene therapy.

XX Example 7; Col 103; 140pp; English.

XX PCR primers AAV70745-46 are used to amplify part of the hepatitis delta
CC virus (HDV) genome. The amplified product is used in the production of
CC the alphavirus vector constructs of the invention. These constructs
CC comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA
CC from the viral cDNA by in vitro transcription, followed by a 5' sequence
CC which initiates transcription of alphavirus RNA, followed by a nucleotide
CC sequence encoding alphavirus nonstructural proteins, a viral junction
CC region which has been inactivated such that viral transcription of a
CC subgenomic fragment is prevented, an internal ribosome entry site or a
CC sequence which promotes ribosome read through between adjacent reading
CC frames, and an alphavirus RNA polymerase recognition sequence. The
CC recombinant alphavirus vectors can be used for gene therapy. (Updated on
CC 20-MAR-2003 to correct PR field.)

XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 11;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCCUCGCGGUNNNNNUGGCGAUGCG 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

Search completed: March 15, 2005, 16:13:02
Job time : 206.285 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 4708233 segs, 24227607955 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	35.4	95.7	57	6	AX012283 Sequence
4	35.4	95.7	57	6	AX012285 Sequence
5	35.4	95.7	57	6	AX012286 Sequence
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8	35.4	95.7	57	6	AX012289 Sequence
9	35.4	95.7	57	6	AX012290 Sequence
10	34	91.9	57	6	AX012284 Sequence
11	30.4	82.2	52	6	AR021007 Sequence
12	30.4	82.2	52	6	AR021047 Sequence
13	30.4	82.2	52	6	AR043422 Sequence
14	30.4	82.2	52	6	AR043462 Sequence
15	30.4	82.2	52	6	AR062337 Sequence
16	30.4	82.2	52	6	AR062377 Sequence
17	30.4	82.2	52	6	AR183796 Sequence
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37	22	59.5	49	6	AR039158 Sequence
38	22	59.5	49	6	AR128882 Sequence
39	22	59.5	49	6	AR165900 Sequence
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SOURCE	other sequences; artificial sequences.				
ORGANISM	Ananvoranich,S., Lafontaine,D. and Perreault,J.P.				
REFERENCE	Nucleic acid enzyme for rna cleavage				
AUTHORS	Patent: WO 9955856-A 53 04-NOV-1999;				
TITLE	ANANVORANICH SIRINAT (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN				
JOURNAL	PIERRE (CA); UNIV SHERBROOKE (CA)				
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VERSION	GI:9998343			
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM				

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other sequences; artificial sequences.
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AUTHORS
Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
JOURNAL
Patent: WO 995856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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DEFINITION Sequence 45 from Patent WO995856.
ACCESSION AX012283
VERSION AX012283.1 GI:9998344
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 995856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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DEFINITION Sequence 47 from Patent WO995856.
ACCESSION AX012285
VERSION AX012285.1 GI:9998346
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 995856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 995856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
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LOCUS AX012286 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 48 from Patent WO995856.
ACCESSION AX012286
VERSION AX012286.1 GI:9998347
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 995856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCGCGGNNNNNUGGCAUGC GCC 37
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DEFINITION Sequence 49 from Patent WO995856.
ACCESSION AX012287
VERSION AX012287.1 GI:9998348
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 995856-A 49 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGUCCACCTCTCCGGGTCGGGCTGGGCAUGC GCC 37
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RESULT 7
LOCUS AX012288 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 50 from Patent WO9955856.
ACCESSION AX012288
VERSION AX012288.1 GI:9998349
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 50 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Location/Qualifiers
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/mol_type="unassigned RNA"
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ORIGIN
Query Match      95.7%; Score 35.4; DB 6; Length 57;
Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGUCCACCTCTCCGGGTCGGGCTGGGCAUGC GCC 37
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RESULT 8
LOCUS AX012289 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION AX012289
VERSION AX012289.1 GI:9998350
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGUCCACCTCTCCGGGTCGGGCTGGGCAUGC GCC 37
Db 1 GGGTCCACCTCTCTCCGGGTCGGGCTGGGCAUGC GCC 37

RESULT 9
LOCUS AX012290 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION AX012290
VERSION AX012290.1 GI:9998351
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 52 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Location/Qualifiers
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/mol_type="unassigned RNA"
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/notes="synthetic nucleic acid"

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Query Match      95.7%; Score 35.4; DB 6; Length 57;
Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

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RESULT 10
LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
Location/Qualifiers
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/notes="synthetic nucleic acid"

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Db 1 GGGTCCACCTCTCTCCGGGTCGGGCTGGGCAUGC 34

RESULT 11
LOCUS AR021007 52 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 40 from patent US 5789245.
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Search completed: March 15, 2005, 18:04:55
Job time : 732.614 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:52:23 ; Search time 241.636 Seconds
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Title: US-09-699-667E-63

Perfect score: 37

Sequence: 1 ggguccaccuccgcgggunnnnngggcaugcc 37

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

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Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	30.4	82.2	52	17	US-10-346-880-80
3	30.4	82.2	52	17	US-10-150-407-40
4	30.4	82.2	52	17	US-10-150-407-80
5	29	78.4	56	10	US-09-507-362-39
6	29	78.4	56	17	US-10-391-441-39
7	22.4	60.5	39	10	US-09-991-262-7
8	22.4	60.5	60	10	US-09-908-975-18325
9	22	59.5	33	10	US-09-864-636A-381
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44	20.2	54.6	43	17	US-10-465-789A-20
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ALIGNMENTS

RESULT 1

US-10-346-880-40
; Sequence 40, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FASTSEQ for Windows Version 3.0

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Sequence 381, App
Sequence 382, App
Sequence 5, Appli
Sequence 1234, Ap
Sequence 9, Appli
Sequence 38, Appl
Sequence 38, Appl
Sequence 704, App
Sequence 6071, Ap
Sequence 33, Appl
Sequence 33, Appl
Sequence 80, Appl
Sequence 45, Appl
Sequence 10, Appl
Sequence 17466, A
Sequence 343874,
Sequence 2, Appli
Sequence 28, Appl
Sequence 85, Appl
Sequence 97, Appl
Sequence 29, Appl
Sequence 118, App
Sequence 9, Appli
Sequence 106, App
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; SEQ ID NO 40
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match      82.2%; Score 30.4; DB 17; Length 52;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGCGGNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

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US-10-346-880-80
; Sequence 80, Application US/10346880
; Publication No. US20030232035A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Ibanez, Carlos E
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; APPLICANT: Belli, Barbara A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
; CURRENT APPLICATION NUMBER: US/10/346,880
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/503,138
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/191,747
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 08/739,199
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

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Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
US-10-346-880-40

Query Match      82.2%; Score 30.4; DB 17; Length 52;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 80, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M
; APPLICANT: Jolly, Douglas J
; APPLICANT: Driver, David A
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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/ APPLICATION NUMBER: US/10/150,407
/ FILING DATE: 17-May-2002
/ CLASSIFICATION: <Unknown>
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/350,522
/ FILING DATE: 08-Jul-1999
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-150-407-80

Query Match      82.2%; Score 30.4; DB 17; Length 52;
Best Local Similarity 59.4%; Pred. No. 2.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNUGGCG 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 5
US-09-507-362-39
; Sequence 39, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
;           Polo, John M.
;           Belli, Barbara A.
;           Schlesinger, Sondra
;           Dryga, Sergey A.
;           Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-150-407-80

Query Match      78.4%; Score 29; DB 17; Length 56;
Best Local Similarity 58.6%; Pred. No. 9.4;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030232058A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
;           Polo, John M.
;           Belli, Barbara A.
;           Schlesinger, Sondra
;           Dryga, Sergey A.
;           Frolov, Ilya
;
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
;
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
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; FILING DATE: 17-Mar-2003
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-391-441-39

Query Match      78.4%; Score 29; DB 17; Length 56;
Best Local Similarity 58.6%; Pred. No. 9.4;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNUGGCGAU 32
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Db 27 TCCACCTCTCGCGGTCCGACCTGGGCAT 55
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; Publication No. US20030041349A1
; GENERAL INFORMATION:
; APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
; TITLE OF INVENTION: Insect Viruses and Their Uses in
; Protecting Plants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/991,262
; FILING DATE: 20-No. US20030041349A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,238
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: US 08/485,355
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/440,522
; FILING DATE: 12-MAY-1995
; APPLICATION NUMBER: US 08/089,372
; FILING DATE: 08-JUL-1993
; APPLICATION NUMBER: AU PL4081/92
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58631-3/RFT/DSS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277239
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-991-262-7

Query Match 50.5%; Score 22.4; DB 10; Length 39;
Best Local Similarity 58.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTUCCUCGCGGUNNNNNNUGGCA 31
Db 16 CTTCTCGCGCGCCGGATGGCA 39

RESULT 8
US-09-908-975-18325/c
; Sequence 18325, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
```

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; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18325
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-908-975-18325

Query Match 60.5%; Score 22.4; DB 10; Length 60;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGUCCACCUCCUGCGGUNNNNNNUGGCAUG 33
Db 53 GGTCCACATCCACACAGATGGCCTTGAGCATG 22

RESULT 9
US-09-864-636A-381/c
; Sequence 381, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwai, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 381
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-864-636A-381

Query Match 59.5%; Score 22; DB 10; Length 33;
Best Local Similarity 53.3%; Pred. No. 4.5e+03;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGUCCACCUCCUGCGGUNNNNNNUGGCA 31
Db 31 GGTCCACCTCCAGAGGAGGTGCGTGGCA 2

RESULT 10
US-09-864-636A-382
; Sequence 382, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwai, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
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Query Match
Best Local Similarity 59.5%; Score 22; DB 10; Length 33;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 382
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-426A-382

Query Match
Best Local Similarity 59.5%; Score 22; DB 10; Length 33;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGUCCACCUCCGCGGUNNNNNNUGGCA 31
||:|||||:| | | | | :|||
Db 3 GGTCCACCTCCAGGAGGTCGGTGGCA 32

RESULT 11
US-09-864-426A-381/c
; Sequence 381, Application US/09864426A
; Publication No. US2004001849A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Ma, Wu Po
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Saizer, Michael
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
; FILE REFERENCE: FORS-04946
; CURRENT APPLICATION NUMBER: US/09/864,426A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 381
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-426A-381

Query Match
Best Local Similarity 59.5%; Score 22; DB 11; Length 33;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGUCCACCUCCGCGGUNNNNNNUGGCA 31
||:|||||:| | | | | :|||
Db 31 GGTCCACCTCCAGGAGGTCGGTGGCA 2

RESULT 12
US-09-864-426A-382
; Sequence 382, Application US/09864426A
; Publication No. US2004001849A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Ma, Wu Po
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Saizer, Michael
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
; FILE REFERENCE: FORS-04946
; CURRENT APPLICATION NUMBER: US/09/864,426A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 382
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-426A-382

Query Match
Best Local Similarity 59.5%; Score 22; DB 11; Length 33;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGUCCACCUCCGCGGUNNNNNNUGGCA 31
||:|||||:| | | | | :|||
Db 3 GGTCCACCTCCAGGAGGTCGGTGGCA 32

RESULT 13
US-10-084-839-381/c
; Sequence 381, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Peggy S.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tssetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 381
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-381

Query Match
Best Local Similarity 59.5%; Score 22; DB 16; Length 33;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 2 GGUCCACCUCCGCGGUNNNNNNUGGCA 31
||:|||||:| | | | | :|||
Db 31 GGTCCACCTCCAGGAGGTCGGTGGCA 2

RESULT 14
US-10-084-839-382
; Sequence 382, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Peggy S.
; APPLICANT: Eis, Peggy S.

APPLICANT: Hall, Jeff G.
APPLICANT: Ip, Hon S.
APPLICANT: Ji, Lin
APPLICANT: Kaiser, Michael
APPLICANT: Kwiatkowski, Jr., Robert W.
APPLICANT: Lukowiak, Andrew A.
APPLICANT: Lyamichev, Victor
APPLICANT: Lymaicheva, Natalie E.
APPLICANT: Ma, WuPo
APPLICANT: Neri, Bruce P.
APPLICANT: Olson, Sarah M.
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Takova, Tsetska Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Vedvik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 382
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-084-839-382

Db 2 UCCACCUCUCGCGGUNNNNN 23

Search completed: March 15, 2005, 21:09:22
Job time : 242.636 secs

Query Match 59.5%; Score 22; DB 16; Length 33;
Best Local Similarity 53.3%; Pred. No. 4.5e+03;
Matches 16; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGUCCACCUCGCGGUNNNNNUGGCGCA 31
|||:|||||:| | | :|||
Db 3 GGTCCACCTCCAGGAGGTGGTGGCGCA 32

RESULT 15
US-09-812-186-5
Sequence 5, Application US/09812186
Patent No. US20020052037A1
GENERAL INFORMATION:
APPLICANT: BEIGELMAN, LEONID
TITLE OF INVENTION: NUCLEIC ACID CATALYSTS COMPRISING L-NUCLEOTIDE ANALOGS
FILE REFERENCE: MBH800-922-A
CURRENT APPLICATION NUMBER: US/09/812,186
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/042,464
PRIOR FILING DATE: 1997-03-31
PRIOR APPLICATION NUMBER: 09/048,825
PRIOR FILING DATE: 1998-03-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 49
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Hepatitis
OTHER INFORMATION: Delta Virus (HDV) Ribozyme.
NAME/KEY: misc_feature
LOCATION: (18)..(24)
OTHER INFORMATION: all n's can represent any one of a, c, g, or u
US-09-812-186-5

Query Match 59.5%; Score 22; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 UCCACCUCGCGGUNNNNN 25

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:20:59 ; Search time 1488.44 Seconds
(without alignments)
946.212 Million cell updates/sec

Title: US-09-699-667E-63

Perfect score: 37

Sequence: 1 ggguccaccucccggunnnnnnugggcaugcgcc 37

Scoring table: IDENTITY NUCDX

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.4	60.5	57	9	CL234247
C 2	21.8	58.9	54	6	CB058194
C 3	21.6	58.4	50	9	CR021509
C 4	21.4	57.8	49	7	H23825
C 5	21.2	57.3	55	1	AA232965
C 6	21.5	56.8	31	1	AI688077
C 7	21.5	56.8	53	9	CR020287
C 8	21.5	56.8	58	9	CR101542
C 9	20.8	56.2	43	9	CG774833
C 10	20.6	55.7	43	1	AI445173
C 11	20.6	55.7	58	1	AI612870
C 12	20.6	55.7	60	1	AA762539
C 13	20.6	55.7	60	6	CD952940
C 14	20.4	55.1	49	1	AA878748
C 15	20.4	55.1	55	6	CB214675
C 16	20.2	54.6	43	1	AA530920
C 17	20.2	54.6	43	8	AZ585629
C 18	20.2	54.6	45	4	BM395132
C 19	20.2	54.6	49	1	AI956143
C 20	20.2	54.6	50	1	AU104848
C 21	20.2	54.6	53	9	CL214958
C 22	20.2	54.6	34	8	AZ340626
C 23	20.2	54.1	38	9	CC799350
C 24	20.2	54.1	53	9	AL953488

C 25	19.8	53.5	49	8	AZ805592
C 26	19.8	53.5	51	8	BH413716
C 27	19.8	53.5	57	9	TA348B10P
C 28	19.8	53.5	58	9	CR360020
C 29	19.6	53.0	32	2	BE782448
C 30	19.6	53.0	55	9	TA234D12P
C 31	19.6	53.0	59	4	BG721695
C 32	19.6	53.0	60	9	BX536340
C 33	19.4	52.4	40	9	CC940306
C 34	19.4	52.4	48	9	CM020376
C 35	19.4	52.4	55	8	AZ804709
C 36	19.4	52.4	57	8	AZ305836
C 37	19.2	51.9	41	8	AZ537682
C 38	19.2	51.9	47	8	AZ806007
C 39	19.2	51.9	47	9	AJ599744
C 40	19.2	51.9	50	1	AU103654
C 41	19.2	51.9	50	1	AU106546
C 42	19.2	51.9	50	1	AU106547
C 43	19.2	51.9	50	1	AU106549
C 44	19.2	51.9	50	9	CR028335
C 45	19.2	51.9	54	1	AJ666287

ALIGNMENTS

RESULT 1
LOCUS CL234247 57 bp DNA linear GSS 08-JAN-2004
DEFINITION 02S0288-04D1-A12 UniformMu MUTAIL Library Zea mays genomic clone
ACCESSION CL234247
VERSION CL234247.1 GI:40778227
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 57)
AUTHORS Lathaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line: 02S0288-04, Primer set: D
Class: transposon insertion site.

FEATURES

source
1..57
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="02S0288-04D1-A12"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 60.5%; Score 22.4; DB 9; Length 57;
Best Local Similarity 53.1%; Pred. No. 5.9e+04;


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/db_xref="taxon:9606"
/clone="IMAGE:668622"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares NhMPu S1"
/notes="Organ: mixed (see Below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not 1;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NhMPu, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

ORIGIN

Query Match 57.8%; Score 21.4; DB 7; Length 49;
Best Local Similarity 52.2%; Pred. No. 1.4e+05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GUCCACUCCUCCGGGUNNNNNN 25
Db 26 GTCCACCTCTCGTGGTGGCGG 48

RESULT 5
AA232965/c
LOCUS AA232965 55 bp mRNA linear EST 06-AUG-1997
DEFINITION zr69a04.s1 Soares NhMPu S1 Homo sapiens cDNA clone IMAGE:668622 3'
similar to SW:UCR3 BOVIN P00130 UBILQUINOL-CYTOCHROME C REDUCTASE
COMPLEX 7.2 KD PROTEIN ;, mRNA sequence.
ACCESSION AA232965
VERSION AA232965.1 GI:1856126
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
AUTHORS Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
JOURNAL WashU-Merck EST Project 1997
COMMENT Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 560 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..55
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:668622"
/lab_host="DH10B"
/clone_lib="Soares NhMPu S1"
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHH19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento

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/db_xref="taxon:9606"
/clone="IMAGE:668622"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares NhMPu S1"
/notes="Organ: mixed (see Below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not 1;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NhMPu, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

ORIGIN

Query Match 57.3%; Score 21.2; DB 1; Length 55;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 17; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 3 GUCCACUCCUCCGGGUNNNNNNUGGCAUGCGC 36
Db 55 GACCACATCTCGAGGGGACGCTGTGGCATCCCC 22

RESULT 6
AI688077/c
LOCUS AI688077 31 bp mRNA linear EST 07-MAR-2000
DEFINITION wa83d03.x1 Soares NFL T_GBC S1 Homo sapiens cDNA clone
IMAGE:2302757 3' similar to SW:EXT1 HUMAN Q16394 EXOSTOSIN-1
;contains MER22.t1 MER22 repetitive element ;, mRNA sequence.
ACCESSION AI688077
VERSION AI688077.1 GI:4899371
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1191 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
source
1..31
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2302757"
/lab_host="DH10B"
/clone_lib="Soares NFL T_GBC S1"
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHH19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento

```


RESULT 10
AI445173/c
LOCUS
DEFINITION
t191e12.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2154478 3'
similar to SW:PRPM_HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO
;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens

REFERENCE
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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/lab_host="DH10B"
/clone_lib="NCI CGAP Col4"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"

ORIGIN
Query Match 55.7%; Score 20.6; DB 1; Length 43;
Best Local Similarity 51.4%; Pred. No. 2.7e+05;
Matches 18; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 3 GUCCACUCCUGCGGNNNNNUGGCAUGCGCC 37
DB 38 GCCCCCCCCCCCGGGGTTTTTTTGGGGGGGCC 4

RESULT 11
AI612870/c
LOCUS
DEFINITION
tx20f12.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2269775 3'
similar to TR:Q40503 Q40503 EXTENSIN. [1] ;contains MSRI.t1 MSRI
repetitive element ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens

REFERENCE
1 (bases 1 to 58)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
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Location/Qualifiers
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/clone="IMAGE:2269775"
/tissue_type="serous papillary carcinoma, high grade, 2
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/lab_host="DH10B"
/clone_lib="NCI CGAP Ut4"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

ORIGIN
Query Match 55.7%; Score 20.6; DB 1; Length 58;
Best Local Similarity 51.9%; Pred. No. 2.7e+05;
Matches 14; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 10 UCCUCGCGGNNNNNUGGCAUGCGC 36
DB 49 TCGTCGCGGAGCAGGAGGTGCATGCGC 23

RESULT 12
AA762539/c
LOCUS
DEFINITION
AA762539 60 bp mRNA linear EST 27-JAN-1998
IMAGE:1228748 5' similar to gb:M95525 Mouse inhibin alpha-subunit
(MOUSE);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
Therrien, B., Wyllie, T., Lehman, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 869 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
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FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:2269775"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
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/clone_lib="NCI CGAP Ut4"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

ORIGIN
Query Match 55.7%; Score 20.6; DB 1; Length 58;
Best Local Similarity 51.9%; Pred. No. 2.7e+05;
Matches 14; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 10 UCCUCGCGGNNNNNUGGCAUGCGC 36
DB 49 TCGTCGCGGAGCAGGAGGTGCATGCGC 23

RESULT 12
AA762539/c
LOCUS
DEFINITION
AA762539 60 bp mRNA linear EST 27-JAN-1998
IMAGE:1228748 5' similar to gb:M95525 Mouse inhibin alpha-subunit
(MOUSE);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
Therrien, B., Wyllie, T., Lehman, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

TITLE
JOURNAL
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

/organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
/dev_stage="4-weeks after germination"
/clone_lib="Oryza minuta HybriZAP-2.1 XR library"
/note="Organ: immature leaf"

ORIGIN

Query Match 55.1%; Score 20.4; DB 6; Length 55;
Best Local Similarity 46.7%; Pred. No. 3.2e+05;
Matches 14; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGUCCACCUCCGCGGNNNNNNNUGGCC 30
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Db 52 GCGTCCACCTCGTCGATGAAGATGATGCC 23

Search completed: March 15, 2005, 20:38:12
Job time : 1492.44 secs

THIS IS A BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 06:19:02 ; Search time 726.693 Seconds
(without alignments)
2467.126 Million cell updates/sec

Title: US-09-699-667E-63
Perfect score: 37
Sequence: 1 ggguccaccuccgcggunnnnugggcaugcgcc 37

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35.4	95.7	37	6	AX012291 Sequence
2	35.4	95.7	57	6	AX012282 Sequence
3	35.4	95.7	57	6	AX012283 Sequence
4	35.4	95.7	57	6	AX012285 Sequence
5	35.4	95.7	57	6	AX012286 Sequence
6	35.4	95.7	57	6	AX012287 Sequence
7	35.4	95.7	57	6	AX012288 Sequence
8	35.4	95.7	57	6	AX012289 Sequence
9	35.4	95.7	57	6	AX012290 Sequence
10	34	91.9	57	6	AX012284 Sequence
11	30.4	82.2	52	6	AR021007 Sequence
12	30.4	82.2	52	6	AR021047 Sequence
13	30.4	82.2	52	6	AR043422 Sequence
14	30.4	82.2	52	6	AR043462 Sequence
15	30.4	82.2	52	6	AR062337 Sequence
16	30.4	82.2	52	6	AR062377 Sequence
17	30.4	82.2	52	6	AR183796 Sequence
18	30.4	82.2	52	6	AR183836 Sequence
19	30.4	82.2	52	6	AR368179 Sequence

20	30.4	82.2	52	6	AR368219 Sequence
21	30.4	82.2	57	6	CQ759677 Sequence
22	30.4	82.2	80	6	I41388 Sequence 16
23	30.4	82.2	83	6	AR123021 Sequence
24	30.4	82.2	84	6	I41385 Sequence 13
25	30.4	82.2	84	6	I41386 Sequence 14
26	30.4	82.2	86	6	I41378 Sequence 6
27	30.4	82.2	90	6	BD226817 Alphaviru
28	30.4	82.2	90	6	AR243300 Sequence
29	30.4	82.2	90	6	AR342596 Sequence
30	30.4	82.2	90	6	AR342597 Sequence
31	30.4	82.2	90	6	AX174838 Sequence
32	30.4	82.2	90	6	AX174839 Sequence
33	30.4	82.2	101	6	AR363756 Sequence
34	30.4	82.2	105	6	A41844 Sequence 25
35	30.4	82.2	105	6	A41849 Sequence 30
36	30.4	82.2	522	14	AB119049 Hepatitis
37	30.4	82.2	523	14	AB119037 Hepatitis
38	30.4	82.2	524	14	AB119032 Hepatitis
39	30.4	82.2	524	14	AB119033 Hepatitis
40	30.4	82.2	524	14	AB119036 Hepatitis
41	30.4	82.2	524	14	AB119041 Hepatitis
42	30.4	82.2	524	14	AB119042 Hepatitis
43	30.4	82.2	524	14	AB119044 Hepatitis
44	30.4	82.2	524	14	AB119045 Hepatitis
45	30.4	82.2	524	14	AB119046 Hepatitis

ALIGNMENTS

RESULT 1	AX012291	Sequence 53 from Patent WO9955856.	37 bp	RNA	linear	PAT 06-SEP-2000
LOCUS	AX012291					
DEFINITION	AX012291					
ACCESSION	AX012291					
VERSION	AX012291.1	GI:9998352				
KEYWORDS		synthetic construct				
SOURCE		other sequences; artificial sequences.				
ORGANISM						
REFERENCE	1	Ananvoranich, S., Lafontaine, D. and Perreault, J.P.				
AUTHORS		Nucleic acid enzyme for rna cleavage				
TITLE		Patent: WO 9955856-A 53 04-NOV-1999;				
JOURNAL		ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN				
PIERRE (CA); UNIV SHERBROOKE (CA)						
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		/organism="synthetic construct"				
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		/db_xref="taxon:32630"				
		/note="synthetic nucleic acid"				

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Best Local Similarity	64.9%;	Pred. No. 3.5;		
Matches	24;	Conservative 12;	Mismatches 1;	Indels 0;
Gaps	0;			
Qy	1	GGGUCCACUCCUGCGGUNNNNUGGCGAUGCGCC	37	
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Db	1	GGGTCCACCTCTCGCGGTCGCACCTGGCATCGGC	37	
		: : : : : : : : : : : : : : : :		
RESULT 2				
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LOCUS	AX012282	Sequence 44 from Patent WO9955856.	57 bp	RNA
DEFINITION	AX012282			
ACCESSION	AX012282			
VERSION	AX012282.1	GI:9998343		
KEYWORDS		synthetic construct		
SOURCE		synthetic construct		
ORGANISM				

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
Nucleic acid enzyme for rna cleavage
Patent: WO 995856-A 44 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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/note="synthetic nucleic acid"
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Best Local Similarity 64.9%; Pred. No. 3.3;
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QY 1 GGGUCCACCUCCUCGCGGNNNNNUGGCAUGCGCC 37
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Db 1 GGGTCCACCTCTCCGGTCCGAGTGGGCATGCGGC 37
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RESULT 3
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LOCUS
DEFINITION
Sequence 45 from Patent WO995856.
ACCESSION
AX012283
VERSION
AX012283.1 GI:9998344
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 995856-A 45 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
Location/Qualifiers
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/note="synthetic nucleic acid"
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Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCCUCGCGGNNNNNUGGCAUGCGCC 37
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Db 1 GGGTCCACCTCTCCGGTCCGAGTGGGCATGCGGC 37
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RESULT 4
AX012285
LOCUS
DEFINITION
Sequence 47 from Patent WO995856.
ACCESSION
AX012285
VERSION
AX012285.1 GI:9998346
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 995856-A 47 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="synthetic nucleic acid"
ORIGIN
Query Match 95.7%; Score 35.4; DB 6; Length 57;
Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCCUCGCGGNNNNNUGGCAUGCGCC 37
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Db 1 GGGTCCACCTCTCCGGTCCGAGTGGGCATGCGGC 37
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RESULT 5
AX012286
LOCUS
DEFINITION
Sequence 48 from Patent WO995856.
ACCESSION
AX012286
VERSION
AX012286.1 GI:9998347
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 995856-A 48 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
Location/Qualifiers
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QY 1 GGGUCCACCUCCUCGCGGNNNNNUGGCAUGCGCC 37
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RESULT 6
AX012287
LOCUS
DEFINITION
Sequence 49 from Patent WO995856.
ACCESSION
AX012287
VERSION
AX012287.1 GI:9998348
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 995856-A 49 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
Location/Qualifiers
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/note="synthetic nucleic acid"
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Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCCUCGCGGNNNNNUGGCAUGCGCC 37
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Db 1 GGGTCCACCTCTCCGGTCCGAGTGGGCATGCGGC 37
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RESULT 7
AX012288
LOCUS
DEFINITION
Sequence 50 from Patent WO995856.
ACCESSION
AX012288
VERSION
AX012288.1 GI:9998349
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 995856-A 50 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
Location/Qualifiers
1..57
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"
ORIGIN
Query Match 95.7%; Score 35.4; DB 6; Length 57;
Best Local Similarity 64.9%; Pred. No. 3.3;
Matches 24; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
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|||||:|||||:|||||:|||||:|||||:|||||
Db 1 GGGTCCACCTCTCCGGTCCGAGTGGGCATGCGGC 37
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ACCESSION AR021007
VERSION AR021007.1 GI:3975622
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J.
and Driver,D.A.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 5789245-A 40 04-AUG-1998;
FEATURES
source
1..52
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/mol_type="unassigned DNA"
ORIGIN
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Best Local Similarity 59.4%; Pred. No. 2.1e+02;
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
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RESULT 14
AR043462
LOCUS AR043462 52 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 80 from patent US 5814482.
ACCESSION AR043462
VERSION AR043462.1 GI:5964470
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 80 29-SEP-1998;
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ORIGIN
Query Match 82.2%; Score 30.4; DB 6; Length 52;
Best Local Similarity 59.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
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DEFINITION Sequence 40 from patent US 5843723.
ACCESSION AR062337
VERSION AR062337.1 GI:5990028
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W.,
Jolly,D.J., Driver,D.A. and Belli,B.A.
TITLE Alphavirus vector constructs
JOURNAL Patent: US 5843723-A 40 01-DEC-1998;
FEATURES
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1..52
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
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Best Local Similarity 59.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCCUGCGGUNNNNNUGGCGAUGC 35
:||||:||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
:||||:||||:||||:||||:||||:||||:
RESULT 13
AR043422
LOCUS AR043422 52 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 40 from patent US 5814482.
ACCESSION AR043422
VERSION AR043422.1 GI:5964430
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
TITLE Eukaryotic layered vector initiation systems
JOURNAL Patent: US 5814482-A 40 29-SEP-1998;
FEATURES
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/organism="unknown"
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	37	AAZ57639	Aaz57639 Nucleotid
2	35.4	95.7	57	AAZ57636	Aaz57636 Trans-act
3	35.4	95.7	57	AAZ57637	Aaz57637 Trans-act
4	34	91.9	57	AAZ57638	Aaz57638 Trans-act
5	30.4	82.2	48	ADR47040	Adr47040 Dengue vi
6	30.4	82.2	48	ADR47040	Adr47040 Dengue vi
7	30.4	82.2	51	AAQ86173	Aaq86173 Primer HD
8	30.4	82.2	52	AAQ86204	Aaq86204 Sindbis/H
9	30.4	82.2	52	AAT31151	Aat31151 HDV rever
10	30.4	82.2	52	AAT30817	Aat30817 HDV riboz
11	30.4	82.2	52	AAV42394	Aav42394 Nested PC
12	30.4	82.2	52	AAV42426	Aav42426 Forward P
13	30.4	82.2	52	AAV60154	Aav60154 Nested PC
14	30.4	82.2	52	AAV60185	Aav60185 Reverse P
15	30.4	82.2	52	AAV70746	Aav70746 Reverse P
16	30.4	82.2	52	AAV70714	Aav70714 Nested pr
17	30.4	82.2	52	AAZ92930	Aaz92930 Hepatitis
18	30.4	82.2	52	AAZ92970	Aaz92970 Hepatitis
19	30.4	82.2	52	AAZ92843	Aaz92843 Hepatitis
20	30.4	82.2	52	AAZ92803	Aaz92803 Hepatitis

21	30.4	82.2	52	6	AAJ38850	Aal38850 Alphaviru
22	30.4	82.2	52	6	AAJ38810	Aal38810 Alphaviru
23	30.4	82.2	52	6	ABK46276	Abk46276 HDV antic
24	30.4	82.2	52	6	ABK46316	Abk46316 Hepatitis
25	30.4	82.2	52	12	ADI30383	Adi30383 Hepatitis
26	30.4	82.2	52	12	ADI30423	Adi30423 Hepatitis
27	30.4	82.2	52	12	ADO13982	Ado13982 Eukaryoti
28	30.4	82.2	52	12	ADO13942	Ado13942 Eukaryoti
29	30.4	82.2	57	12	ADH10551	Adh10551 Hepatitis
30	30.4	82.2	80	2	AAQ53138	Aaq53138 Substrate
31	30.4	82.2	80	2	AAQ53140	Aaq53140 Substrate
32	30.4	82.2	83	5	AAE28121	Aaf28121 HDV riboz
33	30.4	82.2	84	13	ADR47033	Adr47033 Dengue vi
34	30.4	82.2	85	2	AAQ46665	Aaq46665 Self-clea
35	30.4	82.2	86	2	AAQ46663	Aaq46663 Self-clea
36	30.4	82.2	90	2	AAZ76586	Aax76586 Hepatitis
37	30.4	82.2	90	5	AAZ84035	Aaf84035 EPO gene
38	30.4	82.2	90	5	AAZ84036	Aaf84036 EPO gene
39	30.4	82.2	91	8	ABZ82120	Abz82120 Hepatitis
40	30.4	82.2	94	12	ADP96249	Adp96249 HEP rabie
41	30.4	82.2	99	8	ABZ82121	Abz82121 Hepatitis
42	30.4	82.2	567	1	AAZ82174	Aan82174 Clone del
43	30.4	82.2	1369	12	ADH10576	Adh10576 Nucleotid
44	30.4	82.2	1679	1	AAZ82172	Aan82172 cDNA corr
45	30.4	82.2	1688	8	ABZ77701	Abz77701 Nucleotid

ALIGNMENTS

RESULT 1	AAZ57639	AAZ57639 standard; RNA; 37 BP.
ID	AAZ57639	standard; RNA; 37 BP.
XX	AAZ57639;	
AC	AAZ57639;	
XX	05-APR-2000	(first entry)
DT	05-APR-2000	(first entry)
DE	Nucleotide sequence of bimolecular ribozyme Rza fragment.	
XX	Nucleotide sequence of bimolecular ribozyme Rza fragment.	
KW	Bimolecular ribozyme; viral RNA cleavage; Rza fragment;	
KW	inherited disease; ss.	
XX	Synthetic.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FH	Key	Location/Qualifiers
FT	misc_binding	1..6
FT	misc_binding	/tag= a
FT	misc_binding	/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT	misc_binding	/note= "Forms double-stranded region with bases 20-16 of sequence AAZ57640"
FT	stem_loop	7..19
FT	stem_loop	/tag= b
FT	misc_binding	20..25
FT	misc_binding	/tag= c
FT	misc_binding	/bound_moiety= "Ribozyme substrate Pl.1"
FT	misc_binding	/note= "Forms double-stranded region with bases 11-6 of sequence AAZ57641"
FT	misc_binding	30..37
FT	misc_binding	/tag= d
FT	misc_binding	/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT	misc_binding	/note= "Forms double-stranded region with bases 8-1 of sequence AAZ57640"
PN	WO9955856-A2.	
XX	04-NOV-1999.	
PD	04-NOV-1999.	
XX	29-APR-1999;	99WO-CA000391.
PF	29-APR-1999;	99WO-CA000391.
XX	29-APR-1998;	98CA-02230203.
PR	29-APR-1998;	98CA-02230203.
XX	(UYSH) UNIV SHERBROOKE.	
PA	(UYSH) UNIV SHERBROOKE.	

```
XX Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
XX diagnostic and therapeutic applications.
XX
XX Example 5; Fig 4; 52pp; English.
XX
XX This is the nucleotide sequence bimolecular ribozyme RZA fragment. This
XX ribozyme cleaves substrate SP1.1 (see AAZ57641). The invention relates to
XX a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
XX substrate binding portion with the following sequence 3'-UNNXXN-5'. The
XX substrate of the enzyme has the sequence 5'-H'*GNHHN-3'. The binding
XX portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
XX cleavage site of the substrate (cleavage site is represented by *). At
XX least one nucleotide is present 5' to the cleavage site of the substrate
XX sequence. The enzyme of the invention is used to cleave a substrate
XX nucleotide sequence at a specific cleavage site by mixing the substrate
XX with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
XX for example an inherited disease. The enzymes also have other
XX therapeutic, biotechnological and diagnostic applications
XX
XX Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;
XX
Query Match 100.0%; Score 37; DB 3; Length 37;
Best Local Similarity 83.8%; Pred. No. 0.045;
Matches 31; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCCGCGGCGGNNNNNUGGCGCAUGCGCC 37
Db 1 GGGUCCACCUCUCCGCGGCGGCGGCGGCGGCGGCGGCGCC 37
RESULT 2
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
XX
AC AAZ57636;
XX
XX 05-APR-2000 (first entry)
XX
XX Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
XX
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX inherited disease; deltaRzP1.1; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /*tag= a
FT /*note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /*tag= b
FT misc_binding 20..25
FT /*tag= c
FT stem_loop 30..45
FT /*tag= d
FT misc_binding 52..57
FT /*tag= e
FT /*note= "Forms a double stranded region with bases 6-1"
XX
XX WO955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
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PA (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
XX diagnostic and therapeutic applications.
XX
XX Example 1; Fig 1A; 52pp; English.
XX
XX This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
XX cleaves substrate SP1.1 (see AAZ57641). The invention relates to a
XX nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
XX substrate binding portion with the following sequence 3'-UNNXXN-5'. The
XX substrate of the enzyme has the sequence 5'-H'*GNHHN-3'. The binding
XX portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
XX cleavage site of the substrate (cleavage site is represented by *). At
XX least one nucleotide is present 5' to the cleavage site of the substrate
XX sequence. The enzyme of the invention is used to cleave a substrate
XX nucleotide sequence at a specific cleavage site by mixing the substrate
XX with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
XX for example an inherited disease. The enzymes also have other
XX therapeutic, biotechnological and diagnostic applications
XX
XX Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
XX
Query Match 95.7%; Score 35.4; DB 3; Length 57;
Best Local Similarity 81.1%; Pred. No. 0.18;
Matches 30; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCCGCGGCGGNNNNNUGGCGCAUGCGCC 37
Db 1 GGGUCCACCUCUCCGCGGCGGCGGCGGCGGCGGCGCGCC 37
RESULT 3
AAZ57637
ID AAZ57637 standard; RNA; 57 BP.
XX
AC AAZ57637;
XX
XX 05-APR-2000 (first entry)
XX
XX Trans-acting antigenomic delta ribozyme, deltaRzP1.2 nucleotide sequence.
XX
XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX inherited disease; deltaRzP1.2; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 1..6
FT /*tag= a
FT /*note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /*tag= b
FT misc_binding 20..25
FT /*tag= c
FT stem_loop 30..45
FT /*tag= d
FT misc_binding 52..57
FT /*tag= e
FT /*note= "Forms a double stranded region with bases 6-1"
XX
XX WO955856-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
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XX PA (UYSH ) UNIV SHERBROOKE.
XX PF
XX PR
XX PR Perreault J, Ananvoranich S, Lafontaine D;
XX DR WPI; 2000-096791/08.
XX PA
XX PI
XX PI
XX PI
XX DR
XX DR
XX PT
XX PT
XX PS
XX PS
XX CC
XX CC This is the nucleotide sequence of ribozyme deltaRzP1.2. This ribozyme
XX CC cleaves substrate SP1.2 (see AAZ57634). The invention relates to a
XX CC nucleic acid enzyme (e.g. deltaRzP1.2) that is constructed to have a
XX CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
XX CC substrate of the enzyme has the sequence 5'-H'*GNHNN-3'. The binding
XX CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
XX CC cleavage site of the substrate (cleavage site is represented by *). At
XX CC least one nucleotide is present 5' to the cleavage site of the substrate
XX CC sequence. The enzyme of the invention is used to cleave a substrate
XX CC nucleotide sequence at a specific cleavage site by mixing the substrate
XX CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
XX CC for example an inherited disease. The enzymes also have other
XX CC therapeutic, biotechnological and diagnostic applications. Note: This
XX CC sequence is not shown in the specification, but has been derived from the
XX CC deltaRzP1.1 sequence (AAZ57636) shown in figure 1
XX SQ
XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
XX SQ
XX SQ Query Match 95.7%; Score 35.4; DB 3; Length 57;
XX SQ Best Local Similarity 81.1%; Pred. No. 0.18;
XX SQ Matches 30; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
XX SQ
QY 1 GGGUCCACCUCUCCGCGGUNNNNNNUGGCGAUGGCC 37
Db 1 GGGUCCACCUCUCCGCGGUCGCCAGCUGGCGAUGCGC 37

RESULT 4
AAZ57638
ID AAZ57638 standard; RNA; 57 BP.
XX AC
XX AC AAZ57638;
XX DT
XX DT 15-SEP-2003 (revised)
XX DT 05-APR-2000 (first entry)
XX DE
XX DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
XX KW
XX KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX KW inherited disease; ss.
XX OS
XX OS Hepatitis D virus.
XX FH
XX FH Key Location/Qualifiers
XX FT misc_binding 1..6
XX FT /tag= a
XX FT /note= "Forms double stranded region with bases 52-57"
XX FT
XX FT stem_loop 7..19
XX FT /tag= b
XX FT /note= "Forms double stranded region with bases 52-57"
XX FT
XX FT misc_binding 20..25
XX FT /tag= c
XX FT /note= "Forms double stranded region with bases 52-57"
XX FT
XX FT stem_loop 30..45
XX FT /tag= d
XX FT /note= "Forms double stranded region with bases 52-57"
XX FT
XX FT misc_binding 52..57
XX FT /tag= e
XX FT /note= "Forms a double stranded region with bases 6-1"
XX FT
XX FT
XX PN W0955856-A2.
XX XX
XX PD 04-NOV-1999.

XX PA (UYSH ) UNIV SHERBROOKE.
XX PF
XX PR
XX PR Perreault J, Ananvoranich S, Lafontaine D;
XX DR WPI; 2000-096791/08.
XX PA
XX PI
XX PI
XX PI
XX DR
XX DR
XX PT
XX PT
XX PS
XX PS
XX CC
XX CC This is the nucleotide sequence of a trans-acting antigenomic delta
XX CC ribozyme of the invention. This ribozyme cleaves substrate SP1.1 (see
XX CC AAZ57641). The invention relates to a nucleic acid enzyme (e.g.
XX CC deltaRzP1.1) that is constructed to have a substrate binding portion with
XX CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
XX CC sequence 5'-H'*GNHNN-3'. The binding portion of the enzyme (ribozyme)
XX CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
XX CC (cleavage site is represented by *). At least one nucleotide is present
XX CC 5' to the cleavage site of the substrate sequence. The enzyme of the
XX CC invention is used to cleave a substrate nucleotide sequence at a specific
XX CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
XX CC to cleave viral RNA or RNA causing for example an inherited disease. The
XX CC enzymes also have other therapeutic, biotechnological and diagnostic
XX CC applications. (Updated on 15-SEP-2003 to standardise OS field)
XX SQ
XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
XX SQ
XX SQ Query Match 91.9%; Score 34; DB 3; Length 57;
XX SQ Best Local Similarity 82.4%; Pred. No. 0.57;
XX SQ Matches 28; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
XX SQ
QY 1 GGGUCCACCUCUCCGCGGUNNNNNNUGGCGAUGCC 34
Db 1 GGGUCCACCUCUCCGCGGUCGCCAGCUGGCGAUGCC 34

RESULT 5
ADR47040
ID ADR47040 standard; DNA; 48 BP.
XX AC
XX AC ADR47040;
XX DT
XX DT 18-NOV-2004 (first entry)
XX DE
XX DE Dengue virus vaccine oligonucleotide #15.
XX KW
XX KW ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
XX KW preM protein; C protein; NSI protein signal; vaccine; cervical cancer;
XX KW viral disease; antigen; dendritic cell; immune response;
XX KW human papillomavirus.
XX OS
XX OS Unidentified.
XX XX
XX XX W02004072274-A1.
XX XX
XX XX 26-AUG-2004.
XX PD
XX PD 30-JAN-2004; 2004WO-CN000088.
XX PF
XX PF 30-JAN-2003; 2003CN-00115272.
XX PR
XX PR 30-JAN-2003; 2003CN-00115273.
XX XX
XX XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
XX PA (TENG-) TENGGEN BIOMEDICAL CO.
XX PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX XX
XX XX Pang X;

```

XX WPI; 2004-625870/60.
 XX Virus-like particle vaccines containing dengue virus recombinant replicon
 PT as core for carrier, applicable in preventives or/and remedies for tumors
 PT like cervical cancer and viral diseases.
 XX Example 4; SEQ ID NO 37; 38pp; Chinese.
 XX A dengue virus recombinant replicon has a deletion of the complete coding
 CC sequence for preM protein of dengue virus and also includes elements of
 CC e.g. the non-coding region in the whole of the 5'-end, the coding region
 CC of the front 20 amino acids in the C protein, and the coding region of
 CC NS1 protein signal; coding regions of all non-structural proteins. The
 CC obtained vaccines are useful in producing preventives or/and remedies for
 CC cancer like cervical cancer and viral diseases. Such vaccines can
 CC efficiently express antigen in infected cells, which is because dengue
 CC virus can infect dendritic cells, and can effectively present antigen to
 CC provide immunity effect. Different types of dengue virus can be used to
 CC repeatedly produce efficient immune response thereby strengthening the
 CC body's immune system against the pathogen that contains such antigen.
 CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
 CC expressing system using of the full-length dengue virus cDNA clone
 CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
 CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
 CC lines. This sequence corresponds to an oligonucleotide used in the
 CC recombinant replicon of the invention.
 XX
 SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
 Query Match 82.2%; Score 30.4; DB 13; Length 48;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 17 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 48
 RESULT 6
 ADT48965
 ID ADT48965 standard; DNA; 48 BP.
 AC ADT48965;
 XX
 XX 16-DEC-2004 (first entry)
 DT
 XX
 DE PCR primer 5' HDVr, seq id 29.
 DE
 XX
 KW Virucide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;
 KW PCR; primer; ss.
 XX
 OS Viruses.
 XX
 XX WO2004082712-A1.
 PN
 XX
 PD 30-SEP-2004.
 XX
 XX 19-MAR-2004; 2004WO-CN000232.
 PF
 XX
 XX 20-MAR-2003; 2003CN-00115912.
 PR
 XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
 PA (TENG-) TENGGEN BIOMEDICAL CO.
 PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
 XX
 PI Pang X;
 XX
 XX WPI; 2004-699719/68.
 DR
 XX Bivalent vaccines for preventing and treating Japanese (B) encephalitis
 PT and hepatitis B produced by recombinant technique using encephalitis B
 PT virus as vector to express antigen gene of hepatitis B.
 PT

XX Example 8; SEQ ID NO 29; 33pp; Chinese.
 XX The invention relates to a recombinant Japanese encephalitis B virus
 CC constructed from encephalitis B virus and a recombinant genome, where the
 CC genome is inserted with an exogenous nucleotide sequence for
 CC recombination and capable of retaining its self-replication function. The
 CC virus is useful in producing the bivalent vaccines for preventing and
 CC treating Japanese (B) encephalitis and hepatitis B. Such vaccines are
 CC producible at low cost and have high immunosufficiency, in which the
 CC recombinant virus can efficiently express the antigen of hepatitis B
 CC virus with the safety and immunogenicity of attenuated encephalitis B
 CC virus vaccines. The current sequence represents a PCR primer used in an
 CC example from the invention.
 XX
 SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
 Query Match 82.2%; Score 30.4; DB 13; Length 48;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 17 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 48
 RESULT 7
 AAQ86173
 ID AAQ86173 standard; DNA; 51 BP.
 XX
 AC AAQ86173;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-NOV-1995 (first entry)
 XX
 DE Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.
 XX
 KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; Gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX
 OS Synthetic.
 XX
 XX WO9507994-A2.
 PN
 XX
 XX 23-MAR-1995.
 PD
 XX
 PF 15-SEP-1994; 94WO-US010469.
 XX
 XX 15-SEP-1993; 93US-00122791.
 PR
 PR 18-FEB-1994; 94US-00198450.
 XX
 XX (VIAG-) VIAGENE INC.
 PA
 XX
 XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
 PI
 XX WPI; 1995-131362/17.
 DR
 XX New alpha virus vectors for gene therapy - of viral infection, cancer,
 PT auto-immune disease, etc., and as vaccines.
 PT
 XX
 XX Example 2; Page 68; 260pp; English.
 PS
 XX The sequences given in AAQ86167-81 are primers which were used in the
 CC generation of plasmid DNA which initiates Sindbis infection. The
 CC amplified DNA sequences were used in the construction of a eukaryotic
 CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
 CC comprise a 5' sequence capable of initiating transcription of an
 CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
 CC proteins, a viral junction region which has been inactivated such that
 CC viral transcription of the subgenomic fragment is prevented, and an
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the viral

CC junction region prevents transcription of the subgenomic fragment making
 CC vectors such as this suitable for a wide variety of applications, eg.
 CC gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 82.2%; Score 30.4; DB 2; Length 51;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNNUGGCGAUGCG 35
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 Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 8
 AAQ86204
 ID AAQ86204 standard; DNA; 52 BP.
 AC AAQ86204;
 XX
 XX 25-MAR-2003 (revised)
 DT 23-NOV-1995 (first entry)
 XX
 XX Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.
 DE
 XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX
 XX Synthetic.
 OS
 XX WO9507994-A2.
 PN
 XX 23-MAR-1995.
 PD
 XX 15-SEP-1994; 94WO-US010469.
 PF
 XX 15-SEP-1993; 93US-00122791.
 PR 18-FEB-1994; 94US-00198450.
 XX
 XX (VIAG-) VIAGENE INC.
 PA
 XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
 PI WPI; 1995-131362/17.
 DR
 XX New alpha virus vectors for gene therapy - of viral infection, cancer,
 PT auto-immune disease, etc., and as vaccines.
 PT
 XX Example 7; Page 114; 260pp; English.

XX The sequences given in AAQ86200-15 are primers which were used in the
 CC production of alphavirus vectors expressing multiple heterologous genes.
 CC These vectors are eukaryotic layered vector initiation systems (ELVIS)
 CC derived from Sindbis. ELVIS's comprise a 5' sequence capable of
 CC initiating transcription of an alphavirus, a nucleotide sequence encoding
 CC alphavirus non-structural proteins, a viral junction region which has
 CC been inactivated such that viral transcription of the subgenomic fragment
 CC is prevented, and an alphavirus RNA polymerase recognition sequence.
 CC Inactivation of the viral junction region prevents transcription of the
 CC subgenomic fragment making vectors such as this suitable for a wide
 CC variety of applications, eg. gene therapy for the treatment of cystic
 CC fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 82.2%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 9
 AAT31151
 ID AAT31151 standard; DNA; 52 BP.
 AC AAT31151;
 XX
 XX 12-SEP-1996 (first entry)
 DT
 XX HDV reverse primer HDV17-68.
 DE
 XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
 KW polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;
 KW ribozyme; ss.
 XX
 XX Synthetic.
 OS
 XX WO9617072-A2.
 PN
 XX 06-JUN-1996.
 PD
 XX 30-NOV-1995; 95WO-US015490.
 PF
 XX 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00405827.
 XX
 XX (CHIR) CHIRON VIAGENE INC.
 PA
 XX Dubensky TW, Polo JM, Ibanez CE, Chang SM, Jolly DJ, Driver DA;
 PI Belli BA;
 PI
 XX WPI; 1996-277785/28.
 DR
 XX New recombinant alpha-virus vectors - used to develop prods and methods
 PT for use in gene therapy and in the prodn. of vaccines.
 PT
 XX Example 7; Page 120; 256pp; English.

XX Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)
 CC nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)
 CC for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV
 CC (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment
 CC contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping
 CC synthesis is used in a second round of PCR using primers HDV49-XC and
 CC SIN276-SPE. The resulting construct contains the expression cassette
 CC elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction
 CC region/Sindbis structural protein genes/Sindbis 3'-end untranslated
 CC region, designated pds'26s. This was inserted into pCDNA3. Packaging cell
 CC line cassettes were constructed that allow inducible expression of
 CC structural proteins via alphavirus vectors
 XX
 XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 82.2%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGNNNNNNNUGGCGAUGCG 35
 :||||:||||:||||:||||:||||:||||: ||
 Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 10
 AAT30817
 ID AAT30817 standard; DNA; 52 BP.
 AC AAT30817;
 XX
 XX

PT recombinant alpha:virus particles.
 XX Example 7; Col 103; 140pp; English.
 XX
 CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and an
 CC alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the cell,
 CC the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 82.2%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGNNNNNNNNNNUGGCGAUCG 35
 :||||:||||:||||:||||:||||: ||
 Db 1 TCCACCTCTCGCGGTCCGACCTGGCGATCCG 32
 RESULT 13
 AAV60154
 ID AAV60154 standard; DNA; 52 BP.
 XX
 AC AAV60154;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 DT
 DE Nested PCR primer HDV17-68.
 DE
 XX Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 KW
 XX Synthetic.
 OS Hepatitis D virus.
 XX
 XX US5814482-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 30-OCT-1996; 96US-00739158.
 PF
 XX 15-SEP-1993; 93US-00122791.
 XX 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 PI WPI; 1998-541753/46.
 DR
 XX Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 PS Example 3; Col 71-72; 144pp; English.
 PS
 XX PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
 CC ribozyme sequence. The product is used in the course of the invention.

CC The specification describes an eukaryotic layered vector initiation
 CC system, based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
 CC The RNA comprises a vector construct which autonomously amplifies in the
 CC cell and expresses a heterologous nucleic acid sequence which encodes an
 CC antigen or modified form that stimulates an immune response within an
 CC animal. The system is useful for stimulating an immune response to an
 CC antigen by introducing the vector into target cells, preferably by
 CC infection in vivo, especially where the immune response is a cell
 CC mediated, HLA class I-restricted or an HLA class II-restricted immune
 CC response. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 82.2%; Score 30.4; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 11;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACUCCUCCGCGGNNNNNNNNNNUGGCGAUCG 35
 :||||:||||:||||:||||:||||: ||
 Db 1 TCCACCTCTCGCGGTCCGACCTGGCGATCCG 32
 RESULT 14
 AAV60195
 ID AAV60195 standard; DNA; 52 BP.
 XX
 AC AAV60195;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1998 (first entry)
 DT
 DE Reverse PCR primer HDV17-68.
 DE
 XX Eukaryotic layered vector initiation system; stimulate; immune response;
 KW Sindbis; PCR primer; ss.
 KW
 XX Synthetic.
 OS
 XX US5814482-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 30-OCT-1996; 96US-00739158.
 PF
 XX 15-SEP-1993; 93US-00122791.
 XX 18-FEB-1994; 94US-00198450.
 PR 14-SEP-1994; 94WO-US010469.
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00404796.
 XX (POLO/) POLO J M.
 PA (DUBE/) DUBENSKY T W.
 PA (JOLLY) JOLLY D J.
 PA (DRIV/) DRIVER D A.
 XX
 XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
 PI WPI; 1998-541753/46.
 DR
 XX Eukaryotic layered vector initiation system - containing eukaryotic
 PT promoter and heterologous antigen coding sequence, useful for stimulating
 PT immune response.
 XX
 PS Example 5; Col 108; 144pp; English.
 PS
 XX PCR primers AAV60184-85 are used in the course of the invention. The
 CC specification describes an eukaryotic layered vector initiation system,
 CC based on Sindbis. The eukaryotic layered vector initiation system
 CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
 CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.

CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 11;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGUNNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15

AAV70746
ID AAV70746 standard; DNA; 52 BP.

XX AC AAV70746;

XX 20-MAR-2003 (revised)

DT 02-FEB-1999 (first entry)

XX Reverse PCR primer HDV17-68 used to amplify Hepatitis delta virus.

XX Alphavirus vector construct; gene therapy; PCR primer; ss.

XX Synthetic.

OS Hepatitis D virus.

XX US5843723-A.

XX 01-DEC-1998.

PF 30-OCT-1996; 96US-00739167.

XX 15-SEP-1993; 93US-00122791.

PR 18-FEB-1994; 94US-00198450.

PR 30-NOV-1994; 94US-00348472.

PR 20-JAN-1995; 95US-00376184.

PR 15-MAR-1995; 95US-00404796.

XX (CHIR) CHIRON CORP.

XX Chang SMW, Jolly DJ, Dubensky TW, Belli BA, Ibanez CE, Driver DA;

PI Polo JM;

XX WPI; 1999-044581/04.

XX Alphavirus vectors constructs containing a 5' promoter of viral cDNA by
PT in vitro transcription - used in gene therapy.

XX Example 7; Col 103; 140pp; English.

XX PCR primers AAV70745-46 are used to amplify part of the hepatitis delta
CC virus (HDV) genome. The amplified product is used in the production of
CC the alphavirus vector constructs of the invention. These constructs
CC comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA
CC from the viral cDNA by in vitro transcription, followed by a 5' sequence
CC which initiates transcription of alphavirus RNA, followed by a nucleotide
CC sequence encoding alphavirus nonstructural proteins, a viral junction
CC region which has been inactivated such that viral transcription of a
CC subgenomic fragment is prevented, an internal ribosome entry site or a
CC sequence which promotes ribosome read through between adjacent reading
CC frames, and an alphavirus RNA polymerase recognition sequence. The
CC recombinant alphavirus vectors can be used for gene therapy. (Updated on
CC 20-MAR-2003 to correct PR field.)

XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 11;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGUNNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

Search completed: March 15, 2005, 11:20:13
Job time : 204.798 secs

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:18:52 ; Search time 61.3421 Seconds
(without alignments)
986.961 Million cell updates/sec

Title: US-09-699-667E-63

Perfect score: 37
Sequence: 1 99guccaccuccgcggunnnnnnugggcaugcgcc 37

Scoring table: IDENTITY NUCCDX

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/PTCUS COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	30.4	82.2	52	1	US-08-741-881-80
3	30.4	82.2	52	1	US-08-739-158-40
4	30.4	82.2	52	1	US-08-739-158-80
5	30.4	82.2	52	2	US-08-739-167-40
6	30.4	82.2	52	2	US-08-739-167-80
7	30.4	82.2	52	3	US-08-404-796-40
8	30.4	82.2	52	3	US-08-404-796-80
9	30.4	82.2	52	3	US-08-931-869-40
10	30.4	82.2	52	3	US-08-931-869-80
11	30.4	82.2	52	3	US-09-350-399-40
12	30.4	82.2	52	3	US-09-350-399-80
13	30.4	82.2	52	3	US-09-236-140A-40
14	30.4	82.2	52	3	US-09-236-140A-80
15	30.4	82.2	80	1	US-08-238-963A-16
16	30.4	82.2	83	3	US-08-646-695-12
17	30.4	82.2	83	5	PCT-US96-06053-12
18	30.4	82.2	84	1	US-08-238-963A-13
19	30.4	82.2	84	1	US-08-238-963A-14
20	30.4	82.2	86	1	US-08-238-963A-6
21	30.4	82.2	90	4	US-09-554-337-2
22	30.4	82.2	90	4	US-09-733-042-12
23	30.4	82.2	90	4	US-09-733-042-13
24	30.4	82.2	101	6	5225337-2
25	30.4	82.2	101	6	5225337-2
26	30.4	82.2	105	2	US-08-553-619B-25
27	30.4	82.2	105	2	US-08-553-619B-30

Patent No. 5225337

Sequence 25, Appl

Sequence 30, Appl

Sequence 13, Appl

Sequence 12, Appl

Sequence 6, Appl

Sequence 14, Appl

Sequence 13, Appl

Sequence 12, Appl

Sequence 16, Appl

Sequence 12, Appl

Sequence 13, Appl

Sequence 14, Appl

Sequence 6, Appl

Sequence 2, Appl

Sequence 12, Appl

Sequence 13, Appl

Sequence 13, Appl

Patent No. 5225337

Sequence 25, Appl

Sequence 30, Appl

Sequence 13, Appl

Sequence 12, Appl

Sequence 6, Appl

Sequence 14, Appl

Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John W.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EURARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

Query Match 82.2%; Score 30.4; DB 1; Length 52;

Best Local Similarity 59.4%; Pred. No. 4.2;

Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

4 UCCACCUCGCGGNNNNNUGGCAUGCG 35

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Db      1  TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
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RESULT 2
US-08-741-881-80
; Sequence 80, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-80
Query Match      82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4  UCCACCUCUCGCGGNNNNNUGGCGAUGC 35
          :|||||:|||||:|||||:|||||:|||||:
Db      1  TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 4
US-08-739-158-80
; Sequence 80, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80
Query Match      82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY      4  UCCACCUCUCGCGGNNNNNUGGCGAUGC 35
          :|||||:|||||:|||||:|||||:|||||:
Db      1  TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 3
US-08-739-158-40
; Sequence 40, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
```

```
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-739-158-80

Query Match      82.2%; Score 30.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNUGGCGAUGC 35
   :||||:||||:||||:||||:||||:
Db 1 TCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 5
US-08-739-167-40
; Sequence 40, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-40

Query Match      82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNUGGCGAUGC 35
   :||||:||||:||||:||||:||||:
Db 1 TCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 6
US-08-739-167-80
; Sequence 80, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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```
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/739,167
/ FILING DATE: 30-OCT-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-739-167-80

Query Match      82.2%; Score 30.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNUGGCGAUGC 35
   :||||:||||:||||:||||:||||:
Db 1 TCACCTCTCGGGTCCGACCTGGGCATCCG 32

RESULT 7
US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-40

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 8
US-08-404-796-80
Sequence 80, Application US/08404796
Patent No. 6015686
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-404-796-80
Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32
RESULT 9
US-08-931-869-40
Sequence 40, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-40

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGNNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||:
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32
RESULT 10
US-08-931-869-80
Sequence 80, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:

APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-80

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
:||||:||||:||||:||||:||||:||||: ||
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 11
US-09-350-399-40
; Sequence 40, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-350-399-80

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-350-399-40

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
:||||:||||:||||:||||:||||:||||: ||
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 12
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-350-399-80

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
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Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 13

US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A

FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-236-140A-40
Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||: ||
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 14

US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.

Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match 82.2%; Score 30.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGC 35
:|||||:|||||:|||||:|||||:|||||: ||
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 15

US-08-238-963A-16
; Sequence 16, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2086
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,963A


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; FILING DATE: May 5, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/821,155
; FILING DATE: January 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-238-963A-16

Query Match      82.2%; Score 30.4; DB 1; Length 80;
Best Local Similarity 78.1%; Pred. No. 4.6;
Matches 25; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      4 UCCACCUCCUCGCGGUNNNNNUGGCAUGCG 35
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Db      8 UCCACCUCCUCGCGGUGCGACCUCCGCAUCCG 39
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Search completed: March 15, 2005, 15:26:38
Job time : 62.3421 secs

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Result No.	Score	Match	Query #	Length	DB	ID	Description	
1	14.2	71.0	37	1	US-08-612-895A-54	Sequence 54, Appl		
2	14.2	71.0	37	3	US-09-293-293-54	Sequence 54, Appl		
3	14.2	71.0	37	3	US-09-459-553-54	Sequence 54, Appl		
4	14.2	71.0	37	4	US-09-882-246-54	Sequence 54, Appl		
5	14.2	71.0	37	5	PCI-US94-10562A-54	Sequence 54, Appl		
6	13.8	69.0	39	1	US-08-096-027-4	Sequence 4, Appl		
7	13.8	69.0	39	1	US-08-461-725-4	Sequence 4, Appl		
8	13.8	69.0	39	2	US-08-460-981-4	Sequence 4, Appl		
9	13.6	68.0	35	1	US-07-632-905B-80	Sequence 80, Appl		
10	13.6	68.0	35	2	US-08-700-757-80	Sequence 80, Appl		
11	13.6	68.0	35	3	US-09-518-914-33	Sequence 33, Appl		
12	13.6	68.0	43	1	US-07-632-905B-81	Sequence 81, Appl		
13	13.6	68.0	43	2	US-08-700-757-81	Sequence 81, Appl		
14	13.6	68.0	47	1	US-08-171-389-282	Sequence 282, App		
15	13.6	68.0	47	1	US-08-123-936-282	Sequence 282, App		
16	13.6	68.0	47	2	US-08-475-228A-282	Sequence 282, App		
17	13.6	68.0	47	3	US-08-482-080A-282	Sequence 282, App		
18	13.6	68.0	47	3	US-09-354-947-282	Sequence 282, App		
19	13.6	68.0	47	5	PCI-US93-12388-282	Sequence 282, App		
20	13.4	67.0	20	1	US-07-889-651-10	Sequence 10, Appl		
21	13.4	67.0	20	4	US-09-060-299-306	Sequence 306, App		
22	13.4	67.0	20	4	US-09-402-923A-306	Sequence 306, App		
23	13.4	67.0	27	3	US-09-073-492-5	Sequence 5, Appl		
24	13.4	67.0	40	4	US-09-060-299-307	Sequence 307, App		
25	13.4	67.0	40	4	US-09-402-923A-307	Sequence 307, App		
26	13.4	67.0	48	1	US-08-741-881-41	Sequence 41, Appl		
27	13.4	67.0	48	1	US-08-739-158-41	Sequence 41, Appl		

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; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-612-895A-54

Query Match          71.0%; Score 14.2; DB 1; Length 37;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACC 19
    ||||| ||||| |||||
Db 12 GCGCGACGGAUAGGACC 30

RESULT 2
US-09-093-293-54
; Sequence 54, Application US/09093293
; Patent No. 6001577
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: WILLIS, MICHAEL
; APPLICANT: KOCH, TAD
; APPLICANT: RINGQUIST, STEVEN
; APPLICANT: JENSEN, KIRK
; APPLICANT: ATKINSON, BRENT
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF
; TITLE OF INVENTION: LIGANDS BY EXPONENTIAL
; TITLE OF INVENTION: ENRICHMENT: PHOTOSELECTION
; TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND
; TITLE OF INVENTION: SOLUTION SELEX
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,293
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,895
; FILING DATE: 03 August 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10542
; FILING DATE: 18 September 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,935
; FILING DATE: 17 September 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/143,564
; FILING DATE: 25 October 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10 JUNE 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11 JUNE 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17 AUGUST 1992
; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX10/US-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-093-293-54

Query Match          71.0%; Score 14.2; DB 3; Length 37;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACC 19
    ||||| ||||| |||||
Db 12 GCGCGACGGAUAGGACC 30

RESULT 3
US-09-459-553-54
; Sequence 54, Application US/09459553
; Patent No. 6291184
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: WILLIS, MICHAEL
; APPLICANT: KOCH, TAD
; APPLICANT: RINGQUIST, STEVEN
; APPLICANT: JENSEN, KIRK
; APPLICANT: ATKINSON, BRENT
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF
; TITLE OF INVENTION: LIGANDS BY EXPONENTIAL
; TITLE OF INVENTION: ENRICHMENT: PHOTOSELECTION
; TITLE OF INVENTION: OF NUCLEIC ACID LIGANDS AND
; TITLE OF INVENTION: SOLUTION SELEX
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,553
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/093,293
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10542
; FILING DATE: 18 September 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,935
; FILING DATE: 17 September 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/143,564
; FILING DATE: 25 October 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10 JUNE 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11 JUNE 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17 AUGUST 1992
; ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 07/536,428
FILING DATE: 11 JUNE 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17 AUGUST 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/US-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-459-553-54

Query Match 71.0%; Score 14.2; DB 3; Length 37;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGCGAUGGCUAAGGACC 19
Db 12 GCGCGACGGAUAGGAACC 30

RESULT 4

PCT-US94-246-54
Sequence 54, Application US/09882246
Patent No. 6482594
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
WILLIS, MICHAEL
KOCH, TAD
RINGQUIST, STEVEN
JENSEN, KIRK
ATKINSON, BRENT
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF
LIGANDS BY EXPONENTIAL
ENRICHMENT: PHOTOSELECTION
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/882,246
FILING DATE: 14-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,293
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US94/10542
FILING DATE: 18 September 1994
APPLICATION NUMBER: 08/123,935
FILING DATE: 17 September 1993
APPLICATION NUMBER: 08/143,564
FILING DATE: 25 October 1993
APPLICATION NUMBER: 07/714,131
FILING DATE: 10 JUNE 1991

APPLICATION NUMBER: 07/536,428
FILING DATE: 11 JUNE 1990
APPLICATION NUMBER: 07/931,473
FILING DATE: 17 AUGUST 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/US-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-882-246-54

Query Match 71.0%; Score 14.2; DB 4; Length 37;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGCGAUGGCUAAGGACC 19
Db 12 GCGCGACGGAUAGGAACC 30

RESULT 5

PCT-US94-10562A-54
Sequence 54, Application PC/TUS9410562A
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
WILLIS, MICHAEL
KOCH, TAD
RINGQUIST, STEVEN
JENSEN, KIRK
ATKINSON, BRENT
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF
LIGANDS BY EXPONENTIAL
ENRICHMENT: PHOTOSELECTION
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.44 MB
storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10562A
FILING DATE: 16 SEPTEMBER 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: 17 September 1993
APPLICATION NUMBER: 08/143,564
FILING DATE: 25 October 1993
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/PCT
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-10562A-54

Query Match 71.0%; Score 14.2; DB 5; Length 37;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGCGCAAGGCUAAGGACC 19
Db 12 GCGCGCACGAUAGGAACC 30

RESULT 6

US-08-096-027-4
Sequence 4, Application US/08096027
Patent No. 5591632
GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael A.
APPLICANT: Duda, Rosemary B.
APPLICANT: Dewolf, William C.
APPLICANT: Aldovini, Anna
APPLICANT: Young, Richard A.
TITLE OF INVENTION: RECOMBINANT BCG VACCINES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,027
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,334
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,894
FILING DATE: 19-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/03451
FILING DATE: 18-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02962
FILING DATE: 07-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/361,944
FILING DATE: 05-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/223,089
FILING DATE: 22-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/216,390
FILING DATE: 07-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/163,546
FILING DATE: 03-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US88/00614

FILING DATE: 29-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/020,451
FILING DATE: 02-MAR-1987
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI89-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-096-027-4

Query Match 69.0%; Score 13.8; DB 1; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 2;

Qy 4 GCAUGGCUAAGGACCC 20
Db 2 GCATGCCACGAGGATCC 18

RESULT 7

US-08-461-725-4
Sequence 4, Application US/08461725
Patent No. 5776465
GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael A.
APPLICANT: Duda, Rosemary B.
APPLICANT: Dewolf, William C.
APPLICANT: Aldovini, Anna
APPLICANT: Young, Richard A.
TITLE OF INVENTION: RECOMBINANT BCG VACCINES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,725
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,027
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,334
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,894
FILING DATE: 19-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/03451
FILING DATE: 18-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02962
FILING DATE: 07-JUL-1989
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/361,944
; FILING DATE: 05-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/223,089
; FILING DATE: 22-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/216,390
; FILING DATE: 07-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/163,546
; FILING DATE: 03-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US88/00614
; FILING DATE: 29-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/020,451
; FILING DATE: 02-MAR-1987
; APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH189-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-461-725-4

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```

Query Match          69.0%; Score 13.8; DB 1; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      4 GCAUGGCUAAGGACCC 20
        |||:|||||
DB      2 GCATGGCCAAGGATCC 18

```

```

RESULT 8
US-08-460-981-4
; Sequence 4, Application US/08460981
; Patent No. 5830475
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael A.
; APPLICANT: Duda, Rosemary B.
; APPLICANT: DeWolf, William C.
; APPLICANT: Aldovini, Anna
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: RECOMBINANT BCG VACCINES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,981
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,027
; FILING DATE: 22-JUL-1993

```

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,334
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/367,894
; FILING DATE: 19-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/03451
; FILING DATE: 18-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/02962
; FILING DATE: 07-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/361,944
; FILING DATE: 05-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/223,089
; FILING DATE: 22-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/216,390
; FILING DATE: 07-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US88/00614
; FILING DATE: 29-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/020,451
; FILING DATE: 02-MAR-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH189-05A5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-460-981-4

```

```

Query Match          69.0%; Score 13.8; DB 2; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      4 GCAUGGCUAAGGACCC 20
        |||:|||||
DB      2 GCATGGCCAAGGATCC 18

```

```

RESULT 9
US-07-832-905B-80
; Sequence 80, Application US/07832905B
; Patent No. 5580722
; GENERAL INFORMATION:
; APPLICANT: J. Gordon Foulkes, et al.
; TITLE OF INVENTION: Methods of Transcriptionally
; Modulating Expression of Genes Associated With Cardiovascular
; Disease.
; TITLE OF INVENTION: Modulating Expression of Genes Associated With Cardiovascular
; Disease.
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/832,905B
FILING DATE: 19920207
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 26134-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 coop ui
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-832-905B-80

Query Match      68.0%; Score 13.6; DB 1; Length 35;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGCGCAUGGCUAAGGAGCC 20
DB      15 GGGGAAGGCTAAGGAGCC 34

RESULT 10
US-08-700-757-80
Sequence 80, Application US/08700757
Patent No. 5846720
GENERAL INFORMATION:
APPLICANT: J. Gordon Foulkes, et al.
TITLE OF INVENTION: METHODS OF DETERMINING CHEMICALS THAT MODULATE
TITLE OF INVENTION: EXPRESSION OF GENES ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,757
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 26134-HA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
;
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-700-757-80

Query Match      68.0%; Score 13.6; DB 2; Length 35;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGCGCAUGGCUAAGGAGCC 20
DB      15 GGGGAAGGCTAAGGAGCC 34

RESULT 11
US-09-518-914-33/c
Sequence 33, Application US/09518914
Patent No. 6413731
GENERAL INFORMATION:
APPLICANT: Borowsky, Beth E.
APPLICANT: Ogozalek, Kristine L.
APPLICANT: Lakhiani, Parul P.
APPLICANT: Agham, Nika
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REFERENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
CURRENT FILING DATE: 2000-03-03
EARLIER APPLICATION NUMBER: US 09/303,593
EARLIER FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-518-914-33

Query Match      68.0%; Score 13.6; DB 3; Length 35;
Best Local Similarity 70.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGCGCAUGGCUAAGGAGCC 20
DB      26 GTCCATGGCTATGGATCC 7

RESULT 12
US-07-832-905B-81/c
Sequence 81, Application US/07832905B
Patent No. 5580722
GENERAL INFORMATION:
APPLICANT: J. Gordon Foulkes, et al.
TITLE OF INVENTION: Methods of Transcriptionally
TITLE OF INVENTION: Modulating Expression of Genes Associated With Cardiovascular
TITLE OF INVENTION: Disease.
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/832,905B
FILING DATE: 19920207
;
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QY 1 GCGGCAUGGCTUAAGGAGCC 20
Db 28 GGGGAAGGGCTAAGGAGCC 47

Search completed: March 15, 2005, 20:44:24
Job time : 35.2456 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 12:35:18 ; Search time 394.386 Seconds
(without alignments)
2457.248 Million cell updates/sec

Title: US-09-699-667E-64
Perfect score: 20
Sequence: 1 ggcgcaggcuaggagacc 20
Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 1981570

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	18	90.0 57 6	AX012288 Sequence
7	18	90.0 57 6	AX012289 Sequence
8	18	90.0 57 6	AX012290 Sequence
9	17.4	87.0 57 6	AX012284 Sequence
10	17	85.0 18 6	AX012292 Sequence
11	15.8	79.0 29 6	CQ786869 Sequence
12	14.2	71.0 37 6	AR011977 Sequence
13	14.2	71.0 37 6	AR093825 Sequence
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C 24	13.6	68.0	35	6	AR217128	AR217128 Sequence
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ALIGNMENTS

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DEFINITION Sequence 44 from Patent WO955856.
ACCESSION AX012282
VERSION AX012282.1 GI:9998343
KEYWORDS synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich, S., Lafontaine, D. and Perreault, J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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DB 40 CGCATGGCTAGGACCC 57
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LOCUS AX012283 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 45 from Patent WO955856.
ACCESSION AX012283
VERSION AX012283.1 GI:9998344
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM

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other sequences; artificial sequences.
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REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
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Db 40 CGCATGGCTAAGGACCC 57

RESULT 3
AX012285
LOCUS AX012285 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 47 from Patent WO9955856.
ACCESSION AX012285
VERSION AX012285.1 GI:9998346
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCAUGGCUAAGGACCC 20
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DEFINITION Sequence 48 from Patent WO9955856.
ACCESSION AX012286
VERSION AX012286.1 GI:9998347
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AX012287 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 49 from Patent WO9955856.
ACCESSION AX012287
VERSION AX012287.1 GI:9998348
KEYWORDS
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ORGANISM
synthetic construct
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other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 49 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Db 40 CGCATGGCTAAGGACCC 57

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LOCUS AX012288 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 50 from Patent WO9955856.
ACCESSION AX012288
VERSION AX012288.1 GI:9998349
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 50 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Db 40 CGCATGGCTAAGGACCC 57

RESULT 7
LOCUS AX012289 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION AX012289
VERSION AX012289.1 GI:9998350
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
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Db 40 CGCATGGCTAAGGACCC 57

RESULT 8
LOCUS AX012290 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION AX012290
VERSION AX012290.1 GI:9998351
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 52 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Db 40 CGCATGGCTAAGGACCC 57

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LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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RESULT 10
LOCUS AX012292 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 54 from Patent WO9955856.
ACCESSION AX012292
VERSION AX012292.1 GI:9998353
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 54 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Db 2 GCATGGCTAAGGACCC 18

RESULT 11
LOCUS CQ786869 29 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 46 from Patent WO2004021010.

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ACCESSION CQ786869
VERSION CQ786869.1 GI:45721861
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura,Y. and Furukawa,Y.
TITLE Method of diagnosing colon and gastric cancers
JOURNAL Patent: WO 2004021010-A 46 11-MAR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
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Db 9 GCGATGGCTTAGGACGC 27
RESULT 12
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DEFINITION Sequence 54 from patent US 5763177.
ACCESSION AR011977
VERSION AR011977.1 GI:3969967
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Gold,L., Willis,M., Koch,T., Ringquist,S., Jensen,K. and Atkinson,B.
TITLE Systematic evolution of ligands by exponential enrichment:
photonselection of nucleic acid ligands and solution selex
JOURNAL Patent: US 5763177-A 54 09-JUN-1998;
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LOCUS AR093825 37 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 54 from patent US 6001577.
ACCESSION AR093825
VERSION AR093825.1 GI:10020573
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Gold,L., Willis,M., Koch,T., Ringquist,S., Jensen,K. and

Atkinson,B.
TITLE Systematic evolution of ligands by exponential enrichment:
photonselection of nucleic acid ligands and solution selex
JOURNAL Patent: US 6001577-A 54 14-DEC-1999;
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Db 12 GCGCACGGATAAGGAACC 30
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LOCUS AR169735 37 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 54 from patent US 6291184.
ACCESSION AR169735
VERSION AR169735.1 GI:17907643
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Gold,L., Willis,M., Koch,T., Ringquist,S., Jensen,K. and Atkinson,B.
TITLE Systematic evolution of ligands by exponential enrichment:
photonselection of nucleic acid ligands and solution selex
JOURNAL Patent: US 6291184-A 54 18-SEP-2001;
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DEFINITION Sequence 54 from patent US 6482594.
ACCESSION AR255367
VERSION AR255367.1 GI:27304416
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Gold,L., Willis,M., Koch,T., Ringquist,S., Jensen,K. and Atkinson,B.
TITLE Systematic evolution of ligands by exponential enrichment:
photonselection of nucleic acid ligands
JOURNAL Patent: US 6482594-A 54 19-NOV-2002;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	40	13.4	67.0	25	6 ABV86175	Abv86175 Human pp-
	41	13.4	67.0	25	6 ABV86172	Abv86172 Human pp-
	42	13.4	67.0	25	6 ABV86174	Abv86174 Human pp-
	43	13.4	67.0	25	6 ABV86180	Abv86180 Human pp-
	44	13.4	67.0	25	6 ABV86178	Abv86178 Human pp-
C	45	13.4	67.0	27	2 AAV70405	Aav70405 Hepatitis

ALIGNMENTS

RESULT 1
AAZ57640
ID AAZ57640 standard; RNA; 20 BP.
XX
AC AAZ57640;
XX
DT 05-APR-2000 (first entry)
XX
DE Nucleotide sequence of bimolecular ribozyme RzB fragment.
XX
KW Bimolecular ribozyme; viral RNA cleavage; RZA fragment;
KW inherited disease; ss.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT misc_binding 1..8
FT /*tag= a
FT /bound_molec= "Bimolecular ribozyme RzB fragment"
FT /note= "Forms double-stranded region with bases 37-30 of
FT sequence AAZ57639"
FT misc_binding 15..20
FT /*tag= b
FT /bound_molec= "Bimolecular ribozyme RzB fragment"
FT /note= "Forms double-stranded region with bases 6-1 of
FT sequence AAZ57639"
WO9955856-A2.
04-NOV-1999.
29-APR-1999; 99WO-CA000391.
29-APR-1998; 98CA-02230203.
(UYSH) UNIV SHERBROOKE.
Perreault J, Ananvoranich S, Lafontaine D;
WFI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.

```

XX
PS
XX
CC This is the nucleotide sequence of bimolecular ribozyme RzB fragment.
CC relates to a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed
CC to have a substrate binding portion with the following sequence 3'-UNNXXN
CC -5'. The substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The
CC binding portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3'
CC to the cleavage site of the substrate (cleavage site is represented by
CC *). At least one nucleotide is present 5' to the cleavage site of the
CC substrate sequence. The enzyme of the invention is used to cleave a
CC substrate nucleotide sequence at a specific cleavage site by mixing the
CC substrate with the enzyme. The enzyme is used to cleave viral RNA or RNA
CC causing for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
SQ Sequence 20 BP; 4 A; 6 C; 8 G; 0 T; 2 U; 0 Other;
    Query Match      100.0%; Score 20; DB 3; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 20
    |||||
Db 1 GCGCAUGGCUAAGGACCC 20

RESULT 2
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
AC AAZ57636;
XX
DT 05-APR-2000 (first entry)
DE Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzP1.1; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /*tag= a
FT /*note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /*tag= b
FT misc_binding 20..25
FT /*tag= c
FT /*bound_moiety= "SP1.1 substrate (AAZ57641) bases 5-11"
FT stem_loop 30..45
FT /*tag= d
FT misc_binding 52..57
FT /*tag= e
FT /*note= "Forms a double stranded region with bases 6-1"
FT
XX
PN WO955856-A2.
XX
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
PT

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PT
XX
PS
XX
CC This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
CC cleaves substrate SP1.1 (See AAZ57641). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
    Query Match      90.0%; Score 18; DB 3; Length 57;
    Best Local Similarity 100.0%; Pred. No. 14;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCAUGGCUAAGGACCC 20
    |||||
Db 40 CGCAUGGCUAAGGACCC 57

RESULT 3
AAZ57637
ID AAZ57637 standard; RNA; 57 BP.
AC AAZ57637;
XX
DT 05-APR-2000 (first entry)
DE Trans-acting antigenomic delta ribozyme, deltaRzP1.2 nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzP1.2; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /*tag= a
FT /*note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /*tag= b
FT misc_binding 20..25
FT /*tag= c
FT /*bound_moiety= "SP1.2 substrate bases (AAZ57634) 6-11"
FT stem_loop 30..45
FT /*tag= d
FT misc_binding 52..57
FT /*tag= e
FT /*note= "Forms a double stranded region with bases 6-1"
FT
XX
PN WO955856-A2.
XX
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX
XX (UYSH ) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
XX
XX

```

PT New construction of nucleic acid enzyme useful for biotechnological,
XX diagnostic and therapeutic applications.
PS Example 1; Page; 52pp; English.
XX This is the nucleotide sequence of ribozyme deltaRzPl.2. This ribozyme
CC cleaves substrate SPI.2 (see AAZ57634). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzPl.2) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'*GNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications. Note: This
CC sequence is not shown in the specification, but has been derived from the
CC deltaRzPl.1 sequence (AAZ57636) shown in figure 1
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
Query Match 90.0%; Score 18; DB 3; Length 57;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCAUGGCUAAGGACCC 20
Db 40 CGCAUGGCUAAGGACCC 57
RESULT 4
AAZ57638
ID AAZ57638 standard; RNA; 57 BP.
XX
AC AAZ57638;
XX
DT 15-SEP-2003 (revised)
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; ss.
XX
OS Hepatitis D virus.
XX
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /*tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT
FT stem_loop 7..19
FT /*tag= b
FT /note= "Forms double stranded region with bases 52-57"
FT misc_binding 20..25
FT /*tag= c
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 30..45
FT /*tag= d
FT /note= "Forms double stranded region with bases 52-57"
FT misc_binding 52..57
FT /*tag= e
FT /note= "Forms a double stranded region with bases 6-1"
FT
FT
PN WO955856-A2.
XX
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-CA000391.
XX
PR 29-APR-1998; 98CA-02230203.
XX
XX (UYSH) UNIV SHERBROOKE.

PI Perreault J, Ananvoranich S, Lafontaine D;
XX
DR WPI; 2000-096791/08.
XX
PT New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
PS Example 1; Fig 2; 52pp; English.
XX This is the nucleotide sequence of a trans-acting antigenomic delta
CC ribozyme of the invention. This ribozyme cleaves substrate SPI.1 (see
CC AAZ57641). The invention relates to a nucleic acid enzyme (e.g.
CC deltaRzPl.1) that is constructed to have a substrate binding portion with
CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
CC sequence 5'-H'*GNHNN-3'. The binding portion of the enzyme (ribozyme)
CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
CC (cleavage site is represented by *). At least one nucleotide is present
CC 5' to the cleavage site of the substrate sequence. The enzyme of the
CC invention is used to cleave a substrate nucleotide sequence at a specific
CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
CC to cleave viral RNA or RNA causing for example an inherited disease. The
CC enzymes also have other therapeutic, biotechnological and diagnostic
CC applications. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
Query Match 87.0%; Score 17.4; DB 3; Length 57;
Best Local Similarity 94.7%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GCAGUGGCUAAGGACCC 20
Db 39 GCAGUGGCUAAGGACCC 57
RESULT 5
ADL66390
ID ADL66390 standard; DNA; 29 BP.
XX
AC ADL66390;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Nkd1 (CGX7) RT-PCR primer, SEQ ID NO:46.
XX
KW Human; colon and gastric cancer-associated; CGX protein;
KW colorectal cancer; colon cancer; gastric cancer; antisense therapy;
KW gene silencing; drug screening; detection; diagnosis; predisposition;
KW cytostatic; vaccine; CGX7; Nkd1; reverse transcription-PCR; RT-PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO2004021010-A2.
XX
PD 11-MAR-2004.
XX
PF 19-AUG-2003; 2003WO-JP010436.
XX
PR 30-AUG-2002; 2002US-0407338P.
XX
XX (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Furukawa Y;
XX
DR WPI; 2004-239234/22.
XX
PT New CGX polypeptides and polynucleotides, useful in diagnosing, treating
PT and/or preventing colon and gastric cancers.
XX
PS Example 1; SEQ ID NO 46; 228pp; English.
XX

CC The invention relates to human colon and gastric cancer-associated (CGX)
 CC proteins and their encoding nucleic acids which are differentially
 CC expressed in colorectal or gastric cancer. 7 of the 8 CGX genes
 CC identified showed increased expression in colorectal cancers while the
 CC eighth CGX protein, LAPTM4beta (CGX8), showed increased expression in
 CC gastric cancer. Of the 7 colon cancer-associated genes, 2 (Ly6E (CGX6)
 CC and Nkd1 (CGX7)) were known but had not previously been associated with
 CC colon cancer, and 5 were novel. The novel colon cancer-associated genes
 CC are: ARUCL1 (CGX1, ADL66345); C20orf20 (CGX3, ADL66347); CDPUC1 (CGX5,
 CC ADL66349); LEMD1S and LEMD1L (both designated CGX4, ADL66351 and
 CC ADL66353); and NFHL1 (CGX2, ADL66355). The proteins encoded by these
 CC novel genes are given in ADL66346, ADL66348, ADL66350, ADL66352,
 CC and ADL66356. The invention also relates to vectors and host cells
 CC comprising a CGX1-5 nucleic acid; methods for the recombinant production
 CC of CGX1-5; antibodies specific for CGX1-5; antisense polynucleotides or
 CC small interfering RNA (siRNA) targeted to the CGX1-5 or CGX8 genes;
 CC methods of treating or preventing colon or gastric cancer; methods of
 CC screening for compounds for treating or preventing colon or gastric
 CC cancer; DNA arrays comprising CGX1-7 or CGX8 probes; kits for detecting
 CC CGX1-7 or CGX8 polynucleotides or polypeptides; colon cancer reference
 CC expression profiles comprising a pattern of gene expression of two or
 CC more genes selected from CGX1-7; a method for inducing antitumor
 CC immunity; and compositions for the treatment or prevention of colon or
 CC gastric cancer comprising a pharmaceutical amount of a CGX polypeptide or
 CC fragment thereof, an anti-CGX antibody, an antisense polynucleotide, an
 CC siRNA, or a compound identified by screening. The polypeptides,
 CC polynucleotides, compounds, kits or composition are useful in diagnosing
 CC colon and gastric cancer or a predisposition to developing colon or
 CC gastric cancer and in treating or preventing colon and gastric cancer.
 CC The present sequence represents a reverse transcription-PCR (RT-PCR)
 CC primer used in an example of the invention.

XX Sequence 29 BP; 4 A; 9 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 12; Length 29;

Best Local Similarity 78.9%; Pred. No. 1.9e+02;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGCAUGGCUAAGGGACC 20

|||||:|||||
 DB 9 GCGCATGGCTTAGGACGC 27

RESULT 6

AAQ83629

ID AAQ83629 standard; RNA; 37 BP.

XX AC AAQ83629;

XX AC AAQ83629;

DT 25-MAR-2003 (revised)

DT 21-NOV-1995 (first entry)

XX Human immunodeficiency virus type 1 Rev protein RNA ligand 31.

DE Human immunodeficiency virus type 1; HIV-1; Rev protein; RNA ligand 31;

XX Human immunodeficiency virus type 1; HIV-1; Rev protein; RNA ligand 31;

KW photoreactive group; nucleic acid ligand selection; ss.

XX Synthetic.

OS WO9508003-A1.

PN 23-MAR-1995.

XX 16-SEP-1994; 94WO-US010562.

PF 17-SEP-1993; 93US-00123935.

XX 25-OCT-1993; 93US-00143564.

XX (UYRE-) UNIV RES CORP.

XX Gold L, Willis M, Koch T, Ringquist S, Jensen K, Atkinson B;

XX WPI; 1995-131369/17.

XX

XX Selecting nucleic acid ligands for target molecules - by forming
 PT complexes then partitioning by photocrosslinking a selective soln. phase
 PT extension, useful e.g. in diagnosis or treatment of disease.

XX Disclosure; Fig 16; 137pp; English.

XX AAQ83580-Q83630 are HIV-1 Rev protein RNA ligands, which were modified by
 CC the inclusion of a photoreactive group/s to demonstrate a new nucleic
 CC acid (RNA) ligand selection method. Where the ligands with a high affinity
 CC for the target NA (after irradiation) photocrosslink, enabling them to be
 CC separated from the ligands with low affinity for the target NA. (Updated
 CC on 25-MAR-2003 to correct PN field.)

XX Sequence 37 BP; 13 A; 8 C; 11 G; 0 T; 5 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 37;

Best Local Similarity 84.2%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGGACC 19

|||||:|||||
 DB 12 GCGCACGGAUAGGAACC 30

RESULT 7

ACD59856

ID ACD59856 standard; RNA; 17 BP.

XX AC ACD59856;

XX 24-SEP-2003 (first entry)

DE HCV DNzyme substrate sequence #1546.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

KW RNA stability; RNA expression; RNA synthesis; antisense;

KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inosyme; zinzyme;

KW ambarzyme; G-cleaver ribozyme; decoy molecule; aptamer;

KW HBV reverse transcriptase; Enhancer I region; viral replication;

KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;

KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

OS WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PVC/) PAVCO P.

PA (LEEF/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX

PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX
XX Claim 1; Page 261; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGCGCAUGGCUAAGGGA 17
||| |||||
DB 1 GGCGCGUGGCUAAGGGA 17
||| |||||
RESULT 8
AD184300
ID AD184300 standard; RNA; 17 BP.
XX
XX AC AD184300;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE HCV DNazyme substrate sequence #1546.
XX
XX KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
XX
XX OS Hepatitis C virus.
XX
XX PI US2003125270-A1.
XX
XX PN 03-JUL-2003.
XX
XX PP 18-DEC-2000; 2000US-00740332.
XX
XX PR 18-DEC-2000; 2000US-00740332.
XX
XX PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
XX PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX WPI; 2004-031273/03.
XX
XX DR Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX

PS Claim 1; SEQ ID NO 1546; 198pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 12; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGCGCAUGGCUAAGGGA 17
||| |||||
DB 1 GGCGCGUGGCUAAGGGA 17
||| |||||
RESULT 9
AAA92220
ID AAA92220 standard; DNA; 24 BP.
XX
XX AC AAA92220;
XX
XX DT 05-JAN-2001 (first entry)
XX
XX DE Hsc70-PRL1a oligonucleotide primer SEQ ID NO:70.
XX
XX KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytostatic; immunostimulant; cellular immune response inducer;
KW protozoicide; leukaemia; cancer; primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200049041-A1.
XX
XX PD 24-AUG-2000.
XX
XX PF 19-FEB-2000; 2000WO-JP000941.
XX
XX PR 19-FEB-1999; 99JP-00041535.
XX
XX PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
XX PI Shinbara N, Udono H, Yui K;
XX WPI; 2000-543748/49.
XX
XX PT Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer.
XX
XX PS Example 1; Page 17; 72pp; Japanese.
XX
XX The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the ATPase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoacide activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC The present sequence represents a primer which is used in an example from
CC the present invention
XX

```
SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
Query Match          69.0%; Score 13.8; DB 3; Length 24;
Best Local Similarity 76.5%; Pred. No. 2.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGCAUGGCUAAGGACC 19
   |||:|:|:|:|:|
DB 7 CCCATGCTCTAAGGACC 23

RESULT 10
AAA92212
ID AAA92212 standard; DNA; 24 BP.
XX
AC AAA92212;
XX
DT 05-JAN-2001 (first entry)
XX
DE Hsc70-PYE oligonucleotide primer SEQ ID NO:62.
XX
KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytosolic; immunostimulant; cellular immune response inducer;
KW protozoacide; leukaemia; cancer; primer; ss.
XX
OS Synthetic.
XX
PN WO200049041-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-JP000941.
XX
PR 18-FEB-1999; 99JP-00041535.
XX
PA (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI Shinbara N, Udono H, Yui K;
XX
DR WPI; 2000-543748/49.
XX
PT Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer.
XX
PS Example 1; Page 16; 72pp; Japanese.
XX
CC The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the ATPase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoacide activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC The present sequence represents a primer which is used in an example from
CC the present invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
Query Match          69.0%; Score 13.8; DB 3; Length 24;
Best Local Similarity 76.5%; Pred. No. 2.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGCAUGGCUAAGGACC 19
   |||:|:|:|:|:|
DB 7 CCCATGCTCTAAGGACC 23

RESULT 11
AAA92216
ID AAA92216 standard; DNA; 24 BP.
XX
AC AAA92216;
XX
DT 05-JAN-2001 (first entry)
XX
DE Hsc70ATPase domain-PYE oligonucleotide primer SEQ ID NO:66.
XX
KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytosolic; immunostimulant; cellular immune response inducer;
KW protozoacide; leukaemia; cancer; primer; ss.
XX
OS Synthetic.
XX
PN WO200049041-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-JP000941.
XX
PR 19-FEB-1999; 99JP-00041535.
XX
PA (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI Shinbara N, Udono H, Yui K;
XX
DR WPI; 2000-543748/49.
XX
PT Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer.
XX
PS Example 1; Page 16; 72pp; Japanese.
XX
CC The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the ATPase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoacide activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC The present sequence represents a primer which is used in an example from
CC the present invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
Query Match          69.0%; Score 13.8; DB 3; Length 24;
Best Local Similarity 76.5%; Pred. No. 2.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGCAUGGCUAAGGACC 19
   |||:|:~:~:~:~:~
DB 7 CCCATGCTCTAAGGACC 23

RESULT 12
ABQ07884/C
ID ABQ07884 standard; DNA; 24 BP.
XX
AC ABQ07884;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 7875.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
```

```
XX OS Synthetic.
XX PT WO200216649-A2.
XX PN
XX PD 28-FEB-2002.
XX PS
XX PF 27-AUG-2001; 2001WO-US026519.
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX PI WPI; 2002-292068/33.
XX DR
XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX PT target nucleic acid sequence, has different addresses comprising
XX PT different specific capture probes.
XX PS
XX PS Claim 1; Page 186; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX CC and contacting the modified target nucleic acid with (I). The steps of
XX CC above method is useful for detecting a target nucleic acid, which further
XX CC comprises detecting the presence of the modified target nucleic acid
XX SQ Sequence 24 BP; 3 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX OS Synthetic.
XX PT WO200216649-A2.
XX PN
XX PD 28-FEB-2002.
XX PS
XX PF 27-AUG-2001; 2001WO-US026519.
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX PI WPI; 2002-292068/33.
XX DR
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XX PS
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XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX CC and contacting the modified target nucleic acid with (I). The steps of
XX CC above method is useful for detecting a target nucleic acid, which further
XX CC comprises detecting the presence of the modified target nucleic acid
XX SQ Sequence 24 BP; 3 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
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Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX OS Synthetic.
XX PT WO200216649-A2.
XX PN
XX PD 28-FEB-2002.
XX PS
XX PF 27-AUG-2001; 2001WO-US026519.
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX PI WPI; 2002-292068/33.
XX DR
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XX PT Array comprising adapter sequences useful for immobilizing or detecting a
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XX PS
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XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX CC and contacting the modified target nucleic acid with (I). The steps of
XX CC above method is useful for detecting a target nucleic acid, which further
XX CC comprises detecting the presence of the modified target nucleic acid
XX SQ Sequence 24 BP; 8 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX OS Synthetic.
XX PT WO200216649-A2.
XX PN
XX PD 28-FEB-2002.
XX PS
XX PF 27-AUG-2001; 2001WO-US026519.
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX PI WPI; 2002-292068/33.
XX DR
XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX PT target nucleic acid sequence, has different addresses comprising
XX PT different specific capture probes.
XX PS
XX PS Claim 1; Page 90; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX CC and contacting the modified target nucleic acid with (I). The steps of
XX CC above method is useful for detecting a target nucleic acid, which further
XX CC comprises detecting the presence of the modified target nucleic acid
XX SQ Sequence 24 BP; 8 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 6; Length 24;
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Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX OS Synthetic.
XX PT WO200216649-A2.
XX PN
XX PD 28-FEB-2002.
XX PS
XX PF 27-AUG-2001; 2001WO-US026519.
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX PI WPI; 2002-292068/33.
XX DR
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XX PT different specific capture probes.
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XX PS Claim 1; Page 90; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX CC and contacting the modified target nucleic acid with (I). The steps of
XX CC above method is useful for detecting a target nucleic acid, which further
XX CC comprises detecting the presence of the modified target nucleic acid
XX SQ Sequence 24 BP; 8 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX OS Synthetic.
XX PT WO200216649-A2.
XX PN
XX PD 28-FEB-2002.
XX PS
XX PF 27-AUG-2001; 2001WO-US026519.
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX PI WPI; 2002-292068/33.
XX DR
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SQ Sequence 24 BP; 8 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match          69.0%; Score 13.8; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGCAUGGCUAAGGGAC 18
      ||||| ||:|||||
Db      1 GCGCAACGCTAAGGGAC 17

RESULT 15
AAZ31989
ID AAZ31989 standard; DNA; 30 BP.
XX
AC AAZ31989;
XX
XX 28-JAN-2000 (first entry)
XX
XX PCR primer for glucagon-like peptide-1 mutein coding sequence.
XX
XX Glucagon-like peptide-1; GLP-1; mutein; type II diabetes mellitus;
KW insulinotropic peptide; non-insulin dependent diabetes mellitus; obesity;
KW therapy; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9953064-A2.
PN
XX
XX 21-OCT-1999.
PD
XX
XX 13-APR-1999; 99WO-IB000651.
PF
XX
XX 13-APR-1998; 98US-0081562P.
PR
XX 12-APR-1999; 99US-00081562.
PR
XX (MODE-) MODEX THERAPEUTIQUES SA.
PA
XX
XX Thorens B;
PI
XX
XX WPI; 2000-013103/01.
DR
XX
XX Treating type II diabetes mellitus and obesity using glucagon like
PT peptide.
PT
XX
XX Example 4; Page 19; 33pp; English.
PS
XX
XX This sequence represents PCR primer used to isolate DNA encoding a
CC glucagon-like peptide-1 (GLP-1) mutein. The invention relates to a method
CC for treating type II diabetes mellitus, by administering a GLP-1 or a GLP
CC -1 mutein, particularly the mutein GLP-1-Gly8. The GLP-1 mutein is an
CC insulinotropic peptide. The method is used to treat type II diabetes (non
CC -insulin dependent diabetes mellitus) and obesity
XX
XX Sequence 30 BP; 8 A; 5 C; 12 G; 5 T; 0 U; 0 Other;

Query Match          69.0%; Score 13.8; DB 3; Length 30;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 CGCAUGGCUAAGGGACC 19
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Db      14 CGCATGCTAAGGGACC 30

Search completed: March 15, 2005, 16:13:05
Job time : 113.965 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 06:19:02 ; Search time 392.807 Seconds
(without alignments)
2467.126 Million cell updates/sec

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Scoring table: IDENTITY NUCDX
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Listing first 45 summaries

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8: gb_pl.*
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12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	90.0	57	6	AX012282 Sequence
2	18	90.0	57	6	AX012283 Sequence
3	18	90.0	57	6	AX012285 Sequence
4	18	90.0	57	6	AX012286 Sequence
5	18	90.0	57	6	AX012287 Sequence
6	18	90.0	57	6	AX012288 Sequence
7	18	90.0	57	6	AX012289 Sequence
8	18	90.0	57	6	AX012290 Sequence
9	17.4	87.0	57	6	AX012284 Sequence
10	17.4	87.0	11725	6	AR070467 Sequence
11	17.4	87.0	11725	6	I05479 Sequence 13
12	17.4	87.0	11725	6	I07993 Sequence 1
13	17.4	87.0	11725	6	AR390800 Sequence
14	17.4	87.0	11725	6	AR474619 Sequence
15	17.4	87.0	11725	9	HUMPRCA
16	17.4	87.0	13870	6	AX959240 Sequence
17	17.4	87.0	13870	9	AF378903
18	17.4	87.0	172117	10	AC115040
19	17.4	87.0	174539	2	AC113298

C	20	17.4	87.0	205342	9	AC068282	Homo sapi
	21	17.4	87.0	251908	2	AC094522	Rattus no
	22	17	85.0	18	6	AX012292	Sequence
C	23	17	85.0	135005	9	HS860F19	AL035460 Human DNA
	24	17	85.0	236694	2	AC118386	AC118386 Rattus no
C	25	16.8	84.0	468	11	G28378	G28378 human STS S
	26	16.8	84.0	1786	9	AY061883	Homo sapi
	27	16.8	84.0	2604	9	BC051288	Homo sapi
	28	16.8	84.0	2922	6	BD227286	Secreted
C	29	16.8	84.0	60271	2	AC110286	AC110286 Homo sapi
	30	16.8	84.0	120027	2	AC020981	AC020981 Homo sapi
C	31	16.8	84.0	137259	2	AC010392	AC010392 Homo sapi
	32	16.8	84.0	145476	2	AF305874	Homo sapi
C	33	16.8	84.0	148266	2	AC087532	AC087532 Homo sapi
	34	16.8	84.0	149521	2	AC090903	AC090903 Homo sapi
	35	16.8	84.0	154468	2	AC118409	AC118409 Homo sapi
	36	16.8	84.0	158894	2	AC118260	Mus muscu
	37	16.8	84.0	159438	2	AC016621	Homo sapi
C	38	16.8	84.0	160484	9	AC106858	Homo sapi
	39	16.8	84.0	160709	9	AC115837	Homo sapi
	40	16.8	84.0	161649	2	AC023652	AC023652 Homo sapi
C	41	16.8	84.0	163312	9	CNS01DX0	AL138995 Human Chr
	42	16.8	84.0	169773	9	AC007608	AC007608 Homo sapi
C	43	16.8	84.0	170791	9	AC007334	Homo sapi
	44	16.8	84.0	173110	2	AC022102	AC022102 Homo sapi
C	45	16.8	84.0	175177	9	AC020980	Homo sapi

ALIGNMENTS

RESULT 1
AX012282
LOCUS AX012282
DEFINITION Sequence 44 from Patent WO9955856.
ACCESSION AX012282
VERSION AX012282.1 GI:9998343
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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/db_xref="taxon:32630"
/note="synthetic nucleic acid"

ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 57;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCAUGGCUAAGGACCC 20
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Db 40 CGCAGCTAAGGACCC 57
RESULT 2
AX012283
LOCUS AX012283
DEFINITION Sequence 45 from Patent WO9955856.
ACCESSION AX012283
VERSION AX012283.1 GI:9998344
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct

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other sequences; artificial sequences.
1
AUTHORS      Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 45 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY      3 CGCAUGGCUAAGGACCC 20
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Db      40 CGCATGGCTAAGGACCC 57
        ||||:||||:|||||
RESULT 3
LOCUS      AX012285              57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 47 from Patent WO9955856.
ACCESSION  AX012285
VERSION     AX012285.1 GI:9998346
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE      Nucleic acid enzyme for rna cleavage
JOURNAL    Patent: WO 9955856-A 47 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY      3 CGCAUGGCUAAGGACCC 20
        ||||:||||:|||||
Db      40 CGCATGGCTAAGGACCC 57
        ||||:||||:|||||
RESULT 4
LOCUS      AX012286              57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 48 from Patent WO9955856.
ACCESSION  AX012286
VERSION     AX012286.1 GI:9998347
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE      Nucleic acid enzyme for rna cleavage
JOURNAL    Patent: WO 9955856-A 48 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
other sequences; artificial sequences.
1
AUTHORS      Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 45 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
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Query Match      90.0%; Score 18; DB 6; Length 57;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db      40 CGCATGGCTAAGGACCC 57
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RESULT 5
LOCUS      AX012287              57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 49 from Patent WO9955856.
ACCESSION  AX012287
VERSION     AX012287.1 GI:9998348
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE      Nucleic acid enzyme for rna cleavage
JOURNAL    Patent: WO 9955856-A 49 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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        ||||:||||:|||||
Db      40 CGCATGGCTAAGGACCC 57
        ||||:||||:|||||
RESULT 6
LOCUS      AX012288              57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 50 from Patent WO9955856.
ACCESSION  AX012288
VERSION     AX012288.1 GI:9998349
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE      Nucleic acid enzyme for rna cleavage
JOURNAL    Patent: WO 9955856-A 50 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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ORIGIN
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Query Match      90.0%; Score 18; DB 6; Length 57;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCAUGGCUAAGGACCC 20
    ||||:||||:||||:||||
Db 40 CGCATGGCTAAGGACCC 57

RESULT 7
AX012289
LOCUS AX012289 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION AX012289
VERSION AX012289.1 GI:9998350
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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    Location/Qualifiers
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ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 57;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCAUGGCUAAGGACCC 20
    ||||:||||:||||:||||
Db 40 CGCATGGCTAAGGACCC 57

RESULT 8
AX012290
LOCUS AX012290 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION AX012290
VERSION AX012290.1 GI:9998351
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 52 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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    Location/Qualifiers
        1..57
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            /mol_type="unassigned RNA"
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            /note="synthetic nucleic acid"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 57;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCAUGGCUAAGGACCC 20
    ||||:||||:||||:||||
Db 40 CGCATGGCTAAGGACCC 57

RESULT 9
AX012284
LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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            /db_xref="taxon:32630"
            /note="synthetic nucleic acid"

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Query Match      87.0%; Score 17.4; DB 6; Length 57;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCAUGGCUAAGGACCC 20
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Db 39 GGCATGGCTAAGGACCC 57

RESULT 10
AR070467/c
LOCUS AR070467 11725 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5905185.
ACCESSION AR070467
VERSION AR070467.1 GI:7221355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11725)
AUTHORS Garner,I., Cottingham,I.R., Temperley,S.M., Foster,D.C.,
Sprecher,C.A. and Prunkard,D.E.
TITLE Protein C production in non-human transgenic mammals
JOURNAL Patent: US 5905185-A 1 18-MAY-1999;
FEATURES
    source
    Location/Qualifiers
        1..11725
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            /mol_type="unassigned DNA"

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Query Match      87.0%; Score 17.4; DB 6; Length 11725;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
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Db 877 GCGCATGGCAAGGACCC 859

RESULT 11
IO5479/c
LOCUS IO5479 11725 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 13 from Patent EP 0266190.
ACCESSION IO5479
VERSION IO5479.1 GI:591032
KEYWORDS
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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 11725)
TITLE        Foster,D.C., Murray,M.J. and Berkner,K.L.
JOURNAL      Expression of protein C
FEATURES     Patent: EP 0266190-A2 13 04-MAY-1988;
              Location/Qualifiers
                source
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                /mol_type="unassigned DNA"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 11725;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCAUGGCUAAGGACC 19
Db      877 GCGCATGGCAAAGGACC 859
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|||||:|||||

RESULT 12
LOCUS      107993
DEFINITION Sequence 1 from Patent EP 0215548.
ACCESSION 107993
VERSION    107993.1 GI:589294
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11725)
AUTHORS    Murray,M.J., Berkner,K.L., Foster,D.C. and Davie,E.W.
TITLE      Expression of protein C
JOURNAL    Patent: EP 0215548-A1 1 25-MAR-1987;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 11725;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCAUGGCUAAGGACC 19
Db      877 GCGCATGGCAAAGGACC 859
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RESULT 13
LOCUS      AR390800/c
DEFINITION Sequence 50 from patent US 6610906.
ACCESSION  AR390800
VERSION    AR390800.1 GI:40113147
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11725)
AUTHORS    Kurachi,K. and Kurachi,S.
TITLE      Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL    Patent: US 6610906-A 50 26-AUG-2003;
FEATURES   Location/Qualifiers
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            /mol_type="genomic DNA"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 11725;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Kurachi,K. and Kurachi,S.
TITLE        Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL      Patent: US 6610906-A 50 26-AUG-2003;
FEATURES     Location/Qualifiers
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                /mol_type="genomic DNA"

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 11725)
TITLE        Foster,D.C., Murray,M.J. and Berkner,K.L.
JOURNAL      Expression of protein C
FEATURES     Patent: EP 0266190-A2 13 04-MAY-1988;
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Query Match      87.0%; Score 17.4; DB 6; Length 11725;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCAUGGCUAAGGACC 19
Db      877 GCGCATGGCAAAGGACC 859
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RESULT 14
LOCUS      AR474619/c
DEFINITION Sequence 31 from patent US 6692909.
ACCESSION  AR474619
VERSION    AR474619.1 GI:42713733
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11725)
AUTHORS    Lander,E.S., Daley,G.Q., Cargill,M., Ireland,J.S. and Rozen,S.G.
TITLE      Coding sequence polymorphisms in vascular pathology genes
JOURNAL    Patent: US 6692909-A 31 17-FEB-2004;
FEATURES   Location/Qualifiers
            1..11725
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 11725;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCAUGGCUAAGGACC 19
Db      877 GCGCATGGCAAAGGACC 859
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RESULT 15
LOCUS      HUMPRCA/c
DEFINITION Human protein C gene, complete cds.
ACCESSION  M11228
VERSION    M11228.1 GI:190333
KEYWORDS   glycoprotein; protease; protein C; serine protease.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 11725)
REFERENCE  Foster,D.C., Yoshitake,S. and Davie,E.W.
AUTHORS    The nucleotide sequence of the gene for human protein C
TITLE      Proc. Natl. Acad. Sci. U.S.A. 82 (14), 4673-4677 (1985)
JOURNAL    MEDLINE
            85270390
PUBMED     2991887
COMMENT    Original source text: Human DNA, clones PC-lambda-8 and PC-lambda-6.
FEATURES   Location/Qualifiers
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /map="2q13-q21"
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            5450..5584,8253..8395,9269..9386,10516..11105)
            /note="Protein C"
            /codon_start=1
            /protein_id="AAA60166.1"
            /db_xref="GI:190334"
            /translation="MQWTSLLFVATWGISGTPAPLDSVFSSSRAHQVLRIRKAN
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            SLCCGGTGICDIGISFSDCRSGWGRFCOREVSLNCSLDNGGCTHYCLEEVGRRC
            SCAPGYKLGGDILLQCHPAVKPCPGREWKEKRSHLKDTEQDQDQVDPRLIDGWT
            RRGDSFWQVLLDSKKLACGAVLIHPSWLTAAHMCDESKLLVPLGSDVLRWEKWA
            ELDDLKKEVFPNYSKSTTDNDIALHLAQPATLSQTLVIFCLPDSGLAERLNQAG
            QETLVTGWYHSSREKEAKRNRFTVLNFKIPVVPNHNECEVSNMVMNSMLCAGILG

CDS

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join(3520..3630,5093..5117,5210..5347,5450..5584,
8253..8395,9269..9386,10516..11102)
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3464..3630
/number=2
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5210..5347
/number=4
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/note="Proc cds intron D"
5450..5584
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5585..8252
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8253..8395
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8396..9268
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9269..9386
/number=7
9387..10515
/note="Proc cds intron G"
10516..11105
/note="Protein C"
/number=8

ORIGIN 575 bp upstream of StuI site; chromosome 2q14-q21.

Query Match 87.0%; Score 17.4; DB 9; Length 11725;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGACC 19
|||:|||||
DB 877 GGCGCATGGCAAGGACC 859

Search completed: March 15, 2005, 12:35:06
Job time : 397.807 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:20:59 ; Search time 804.561 Seconds
(without alignments)
946.212 Million cell updates/sec

Title: US-09-699-667E-64

Perfect score: 20
Sequence: 1 ggcgaugcuaaggacc 20

Scoring table: IDENTITY NUCDX

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description	
		Match	Length				
1	13.6	68.0	27	4	BM395243	50072-2-8	
2	13.6	68.0	51	9	BX291747	Arabidops	
3	12.8	64.0	34	8	AZ876899	2M0192C06	
C	12.8	64.0	40	1	AI316323	uJ99b12.y	
5	12.8	64.0	40	9	AL763075	Arabidops	
6	12.6	63.0	23	4	BM394673	50072-2-5	
7	12.6	63.0	27	4	BM395141	50072-2-7	
8	12.6	63.0	42	9	BX897261	Arabidops	
9	12.6	63.0	46	9	BX292021	Arabidops	
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C	11	12.6	63.0	50	1	AU102715	AU102715
C	12	12.6	63.0	50	1	AU102717	AU102717
C	13	12.6	63.0	50	1	AU102718	AU102718
C	14	12.6	63.0	52	4	BM393985	50072-2-1
15	12.6	63.0	54	9	AL940566	Arabidops	
C	16	12.6	63.0	60	9	CL211870	W084D04 G
C	17	12.4	62.0	57	8	AZ919092	1006013H0
C	18	12.2	61.0	26	8	AZ804424	2M0605C11
C	19	12.2	61.0	57	6	CB227505	1Ru40D12
C	20	12.2	61.0	58	9	CL183540	Forward s
C	21	12	60.0	29	9	CL983097	GC0336 TI
22	12	60.0	39	8	AZ817621	2M0087M12	
C	23	12	60.0	43	8	CC020441	3591_1_19
C	24	12	60.0	43	8	CC183341	XE744 Bay

25	12	60.0	46	1	AI124043	AI124043	qa94g11..s
C 26	12	60.0	50	1	AU103253	AU103253	
C 27	12	60.0	50	1	AU103254	AU103254	
C 28	12	60.0	50	1	AU103255	AU103255	
C 29	12	60.0	50	1	AU103256	AU103256	
C 30	12	60.0	50	1	AU103257	AU103257	
C 31	12	60.0	50	1	AU103258	AU103258	
C 32	12	60.0	50	1	AU103259	AU103259	
C 33	12	60.0	50	1	AU103260	AU103260	
C 34	12	60.0	50	1	AU103261	AU103261	
C 35	12	60.0	50	1	AU103262	AU103262	
C 36	12	60.0	50	1	AU103263	AU103263	
C 37	12	60.0	50	1	AU103264	AU103264	
C 38	12	60.0	50	1	AU103265	AU103265	
C 39	12	60.0	50	1	AU103266	AU103266	
C 40	12	60.0	50	1	AU103267	AU103267	
C 41	12	60.0	50	1	AU103268	AU103268	
C 42	12	60.0	50	1	AU103269	AU103269	
C 43	12	60.0	50	1	AU103270	AU103270	
C 44	12	60.0	50	1	AU103271	AU103271	
C 45	12	60.0	50	1	AU103272	AU103272	

ALIGNMENTS

RESULT 1
LOCUS BM395243 27 bp mRNA linear EST 17-JAN-2002
DEFINITION 50072-2-8-B11.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395243
VERSION BM395243.1 GI:18195296
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
REFERENCE 1 (bases 1 to 27)
AUTHORS Turkewitz A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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/mol_type="mRNA"
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/notes="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 68.0%; Score 13.6; DB 4; Length 27;
Best Local Similarity 70.0%; Pred. No. 3.3e+04;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 GCGCAUGGCUAAGGACCC 20
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Db 5 GCGCAATGGGTACGGGCCC 24
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RESULT 2


```

RESULT 4
AL763075/c
LOCUS
DEFINITION
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    u99b12.y1 Schiller mouse MAC13 Mus musculus cDNA clone
    IMAGE:1958015 similar to TR:035934 O35934 CLN3. ; mRNA
    sequence.
ACCESSION
AL763075
VERSION
AL763075.1
KEYWORDS
    GSS.
SOURCE
    Arabidopsis thaliana (thale cress)
    Arabidopsis thaliana
    Arabidopsis thaliana
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
    Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
    GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
    the identification of T-DNA insertion mutants in Arabidopsis
    thaliana
    Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL
MEDLINE
22755829
PUBMED
12874060
REFERENCE
2
    Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
    Weisshaar, B.
    An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
    flanking sequence tag-based reverse genetics
    Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL
MEDLINE
23117147
PUBMED
14756321
REFERENCE
3
    Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
    Weisshaar, B.
    High-throughput generation of sequence indexes from T-DNA
    mutagenized Arabidopsis thaliana lines
    Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL
PUBMED
14682050
REFERENCE
4
    (bases 1 to 40)
    Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
    Direct Submission
    Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
    Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
    This sequence has been recovered from the left border of the T-DNA.
    It indicates an insertion close to or within gene At2g21630.
    Details on the protocols used for generation of the sequence are
    described in References 1-3. The sequences are generated at the MPI
    for Plant Breeding Research in the context of the GABI-Kat project.
    GABI-Kat is part of the German Plant Genomics program designated
    'GABI'. Information on line availability can be found at:
    http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
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    /db_xref="taxon:3702"
    /clone="GK-032C06-014864"
    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Col-0"
    /note="PCR was performed on DNA from Arabidopsis thaliana
    plants (T1) which were transformed with the T-DNA from
    vector pAC106 (GenBank accession number: AJ537513). The
    lines contain one or more T-DNA insertions. The DNA
    fragment(s) resulting from the PCR were directly sequenced
    to determine the genomic sequence flanking the insertion.
    T-DNA derived sequences were removed."
ORIGIN
    Query Match 64.0%; Score 12.8; DB 1; Length 40;
    Best Local Similarity 75.0%; Pred. No. 8.7e+04;
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Db 26 GAGCATGGCTTAGGA 11

RESULT 5
AL763075
LOCUS
DEFINITION
    40 bp DNA linear GSS 01-APR-2004
    Arabidopsis thaliana T-DNA flanking sequence GK-032C06-014864,

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genomic survey sequence.
AL763075
VERSION
AL763075.1
KEYWORDS
    GSS.
SOURCE
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    Arabidopsis thaliana
    Arabidopsis thaliana
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    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
    Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
    GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
    the identification of T-DNA insertion mutants in Arabidopsis
    thaliana
    Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL
MEDLINE
22755829
PUBMED
12874060
REFERENCE
2
    Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
    Weisshaar, B.
    An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
    flanking sequence tag-based reverse genetics
    Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL
MEDLINE
23117147
PUBMED
14756321
REFERENCE
3
    Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
    Weisshaar, B.
    High-throughput generation of sequence indexes from T-DNA
    mutagenized Arabidopsis thaliana lines
    Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL
PUBMED
14682050
REFERENCE
4
    (bases 1 to 40)
    Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
    Direct Submission
    Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
    Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
    This sequence has been recovered from the left border of the T-DNA.
    It indicates an insertion close to or within gene At2g21630.
    Details on the protocols used for generation of the sequence are
    described in References 1-3. The sequences are generated at the MPI
    for Plant Breeding Research in the context of the GABI-Kat project.
    GABI-Kat is part of the German Plant Genomics program designated
    'GABI'. Information on line availability can be found at:
    http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
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    /db_xref="taxon:3702"
    /clone="GK-032C06-014864"
    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Col-0"
    /note="PCR was performed on DNA from Arabidopsis thaliana
    plants (T1) which were transformed with the T-DNA from
    vector pAC106 (GenBank accession number: AJ537513). The
    lines contain one or more T-DNA insertions. The DNA
    fragment(s) resulting from the PCR were directly sequenced
    to determine the genomic sequence flanking the insertion.
    T-DNA derived sequences were removed."
ORIGIN
    Query Match 64.0%; Score 12.8; DB 9; Length 40;
    Best Local Similarity 75.0%; Pred. No. 8.7e+04;
    Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAUGGCUAAGGACCC 20
    |||||:|||||
Db 25 CATGGCTATGGATCC 40

RESULT 6

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/clone="GK-765D01-023592"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

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ORIGIN

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Query Match      63.0%; Score 12.6; DB 9; Length 42;
Best Local Similarity 68.4%; Pred. No. 1.1e+05;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCGCAUGGCUAAGGACCC 20
    |||:|:|:|:|:|:|
Db 16 GCCCATGCTATGGGATCC 34

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RESULT 9

```

BX292021          46 bp  DNA  linear  GSS 02-APR-2004
LOCUS             Arabidopsis thaliana T-DNA flanking sequence GK-450B01-019252,
DEFINITION        Genomic survey sequence.
ACCESSION         BX292021
VERSION           BX292021.1 GI:28891017
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Arabidopsis thaliana

```

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

REFERENCE

```

1 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weissshaar, B.
  GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
  the identification of T-DNA insertion mutants in Arabidopsis
  thaliana
  Bioinformatics 19 (11), 1441-1442 (2003)

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JOURNAL

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MEDLINE           22755829
PUBMED            12874060

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REFERENCE

```

2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
  Weissshaar, B.
  An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
  flanking sequence tag-based reverse genetics
  Plant Mol. Biol. 53 (1-2), 247-259 (2003)
  23117147
  14756321

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REFERENCE

```

3 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
  Weissshaar, B.
  High-throughput generation of sequence indexes from T-DNA
  mutagenized Arabidopsis thaliana lines
  Biotechniques 35 (6), 1164-1168 (2003)
  14682050

```

REFERENCE

```

4 Li, Y., Rosso, M.G., Strizhov, N. and Weissshaar, B.
  Direct Submission
  Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
  Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
  This sequence has been recovered from the left border of the T-DNA.
  It indicates an insertion within the locus defined by BAC clone
  T6G15. Details on the protocols used for generation of the sequence
  are described in References 1-3. The sequences are generated at the
  MPI for Plant Breeding Research in the context of the GABI-Kat
  project. GABI-Kat is part of the German Plant Genomics program
  designated 'GABI'. Information on line availability can be found
  at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

```

JOURNAL

```

PUBMED            14682050

```

AUTHORS

```

TITLE             High-throughput generation of sequence indexes from T-DNA
  mutagenized Arabidopsis thaliana lines
  Biotechniques 35 (6), 1164-1168 (2003)
  14682050

```

FEATURES

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source            Location/Qualifiers
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/organism="Arabidopsis thaliana"

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FEATURES

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source            Location/Qualifiers
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FEATURES

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source            Location/Qualifiers
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/organism="Arabidopsis thaliana"

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FEATURES

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source            Location/Qualifiers
1..46
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/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-450B01-019252"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

```

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Query Match      63.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 68.4%; Pred. No. 1.1e+05;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:|:|:|:|:|
Db 14 GCGCGTTGGCTATGGGATC 32

```

ORIGIN

```

Query Match      63.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 68.4%; Pred. No. 1.1e+05;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:~|:|:|:|:|
Db 14 GCGCGTTGGCTATGGGATC 32

```

RESULT 10

```

AU102714/c        50 bp  mRNA  linear  EST 28-JAN-2004
LOCUS             AU102714 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION        CAS02037, mRNA sequence.
ACCESSION         AU102714
VERSION           AU102714.1 GI:13552235
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072

```

JOURNAL

```

MEDLINE           11375929
PUBMED            11375929

```

REFERENCE

```

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

```

FEATURES

```

source            Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS02037"
/clone_lib="Sugano Homo sapiens cDNA library"

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Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:|:|:|:|:|
Db 50 GCGCCATGGCGGCGGATCC 32

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ORIGIN

```

Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:|:|:|:|:|
Db 50 GCGCCATGGCGGCGGATCC 32

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ORIGIN

```

Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:~|:|:|:|:|
Db 50 GCGCCATGGCGGCGGATCC 32

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ORIGIN

```

Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:~|:~|:~|:~|
Db 50 GCGCCATGGCGGCGGATCC 32

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ORIGIN

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Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:~|:~|:~|:~|
Db 50 GCGCCATGGCGGCGGATCC 32

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ORIGIN

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Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGCAUGGCUAAGGACCC 19
    |||:~|:~|:~|:~|
Db 50 GCGCCATGGCGGCGGATCC 32

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```

AUI02715/c
LOCUS      AUI02715      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS08445, mRNA sequence.
ACCESSION  AUI02715      GI:13552236
VERSION     AUI02715.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota.T., Isogai.T., Tanaka.T., Morishita,S., Okubo,K.,
            Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL     11375929
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="CAS08445"
     clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGCGCAUGGCUAAGGGACC 19
        ||| ||| ||| ||| |||
Db      42  GGCCCATGGCGAGGGTCC 24

RESULT 12
AUI02717/c
LOCUS      AUI02717      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01595, mRNA sequence.
ACCESSION  AUI02717      GI:13552238
VERSION     AUI02717.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota.T., Isogai.T., Tanaka.T., Morishita,S., Okubo,K.,
            Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL     11375929
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp

```

```

Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="KAT01595"
     clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGCGCAUGGCUAAGGGACC 19
        ||| ||| ||| ||| |||
Db      49  GGCCCATGGCGAGGGTCC 31

RESULT 13
AUI02718/c
LOCUS      AUI02718      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT06130, mRNA sequence.
ACCESSION  AUI02718      GI:13552239
VERSION     AUI02718.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota.T., Isogai.T., Tanaka.T., Morishita,S., Okubo,K.,
            Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL     11375929
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="KAT06130"
     clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      63.0%; Score 12.6; DB 1; Length 50;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGCGCAUGGCUAAGGGACC 19
        ||| ||| ||| ||| |||
Db      50  GGCCCATGGCGAGGGTCC 32

RESULT 14
BM393985
LOCUS      BM393985      52 bp      mRNA      linear      EST 17-JAN-2002

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DEFINITION 50072-2-12-C08.r.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION  BM393985
VERSION     BM393985.1  GI:18194038
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
REFERENCE  1 (bases 1 to 52)
AUTHORS    Frankel,J., and Klobucher,L.,
            Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,B., Kirk,K.E.,
            EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished (2002)
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL    Contact: Turkewitz AP
COMMENT    Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..52
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
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                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /notes="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      63.0%; Score 12.6; DB 4; Length 52;
Best Local Similarity 58.4%; Pred. No. 1.1e+05;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY  2  GCGCAUGGCUAAGGGACCC 20
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DB   8  GCGAATGGGTACGGGCCCC 26

RESULT 15
AL940566
LOCUS      AL940566
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-249D07-01444,
            genomic survey sequence.
ACCESSION  AL940566
VERSION    AL940566.1  GI:24397015
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
            1
REFERENCE  1
AUTHORS    Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
TITLE      GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
JOURNAL    Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE    22755829
PUBMED     12874060
REFERENCE  2
AUTHORS    Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weissshaar,B.
TITLE      An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics
JOURNAL    Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE    23117147
PUBMED     14756321
REFERENCE  3

```

```

AUTHORS    Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
            Weissshaar,B.
TITLE      High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
JOURNAL    Biotechniques 35 (6), 1164-1168 (2003)
PUBMED     14682050
REFERENCE  4 (bases 1 to 54)
AUTHORS    Rosso,M.G., Li,Y., Strizhov,N. and Weissshaar,B.
TITLE      Direct Submission
JOURNAL    Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
            Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT    This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion close to or within gene At2g34400.
            Details on the protocols used for generation of the sequence are
            described in References 1-3. The sequences are generated at the MPI
            for Plant Breeding Research in the context of the GABI-Kat project.
            GABI-Kat is part of the German Plant Genomics program designated
            'GABI'. Information on line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
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                     /clone_lib="GK-249D07-01444"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pCl61 (GenBank accession number: AU537514). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."

ORIGIN
Query Match      63.0%; Score 12.6; DB 9; Length 54;
Best Local Similarity 73.7%; Pred. No. 1.1e+05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY  2  GCGCAUGGCUAAGGGACCC 20
    ||| | | | | | | | | |
DB   24 GTGCAAGGCTATGGGATCC 42

Search completed: March 15, 2005, 20:38:15
Job time : 807.561 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 01:00:51 ; Search time 110.702 Seconds
(without alignments)
1069.494 Million cell updates/sec

Title: US-09-699-667E-64

Perfect score: 20
Sequence: 1 ggcgcgaugcuaaggagacc 20

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	Aaz57640 Nucleotid
2	18	90.0	57	3	Aaz57636 Trans-act
3	18	90.0	57	3	Aaz57637 Trans-act
4	17.4	87.0	57	3	Aaz57638 Trans-act
5	17.4	87.0	11715	1	Aan81564 Genomic s
6	17.4	87.0	11724	1	Aan70102 Complete
7	17.4	87.0	11724	4	Aah57497 Human liv
8	17.4	87.0	11725	2	Aat32796 Human pro
9	17.4	87.0	11725	2	Aat79723 Human pro
10	17.4	87.0	11725	2	Aaz32179 Human pro
11	17.4	87.0	11725	4	Aaf54051 Human pro
12	17.4	87.0	13870	12	Aal56352 Human pro
13	17	85.0	20188	12	Adh33950 Human CDN
14	17	85.0	20190	10	Adc71539 Human NOV
15	17	85.0	135005	12	Adq19501 Human sof
16	16.8	84.0	1859	3	Aal51511 Human Nkd
17	16.8	84.0	2922	3	Aal16664 Human sec
18	16.8	84.0	348101	12	Adq97146 Human can
19	16.4	82.0	1380	5	Aah67868 C glutami
20	16.4	82.0	1543	10	Add13201 C. glutam

C	21	16.4	82.0	349980	5	Aah68533	Aah68533 C glutami
C	22	15.8	79.0	29	12	AdL66390	AdL66390 Human Nkd
C	23	15.8	79.0	770	5	Aaf93971	Aaf93971 Primer sp
C	24	15.8	79.0	1089	11	ABD16174	ABD16174 Pseudomon
C	25	15.8	79.0	1482	11	ABD16052	ABD16052 Pseudomon
C	26	15.8	79.0	2320	3	AAC58107	Aac58107 Human PRO
C	27	15.8	79.0	2320	3	AAA37101	Aaa37101 Human PRO
C	28	15.8	79.0	2320	4	AAF54401	Aaf54401 Primer #8
C	29	15.8	79.0	2320	9	ACD68440	AcD68440 Novel hum
C	30	15.8	79.0	2320	9	ACH04542	ACH04542 Human CDN
C	31	15.8	79.0	2320	9	ACD68086	AcD68086 Novel hum
C	32	15.8	79.0	2320	10	ADC18150	AdC18150 Human PRO
C	33	15.8	79.0	2320	10	ADD70796	AdD70796 Human CDN
C	34	15.8	79.0	2320	10	ADD39873	AdD39873 Human CDN
C	35	15.8	79.0	2320	10	ADD70319	AdD70319 Human CDN
C	36	15.8	79.0	2320	10	ADD38440	AdD38440 Human CDN
C	37	15.8	79.0	2320	10	ADD39396	AdD39396 Human CDN
C	38	15.8	79.0	2320	10	ADD38919	AdD38919 Human CDN
C	39	15.8	79.0	2320	10	ADD40350	AdD40350 Human CDN
C	40	15.8	79.0	2320	10	ADE50571	Ade50571 Human CDN
C	41	15.8	79.0	2320	10	ADE20183	Ade20183 Human CDN
C	42	15.8	79.0	2320	10	ADE50094	Ade50094 Human CDN
C	43	15.8	79.0	2320	10	ADE21652	Ade21652 Human CDN
C	44	15.8	79.0	2320	10	ADF30077	AdF30077 Human CDN
C	45	15.8	79.0	2320	10	ADF55970	AdF55970 Human CDN

ALIGNMENTS

RESULT 1
AAZ57640
ID AAZ57640 standard; RNA; 20 BP.
XX
AC AAZ57640;
XX
DT 05-APR-2000 (first entry)
DE Nucleotide sequence of bimolecular ribozyme RzB fragment.
KW Bimolecular ribozyme; viral RNA cleavage; RzA fragment;
KW inherited disease; ss.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..8
FT /tag= a
FT /bound moiety= "Bimolecular ribozyme RzB fragment"
FT /notes= "Forms double-stranded region with bases 37-30 of
sequence AAZ57639"
FT misc_binding 15..20
FT /tag= b
FT /bound moiety= "Bimolecular ribozyme RzB fragment"
FT /notes= "Forms double-stranded region with bases 6-1 of
sequence AAZ57639"

WO9955856-A2.

04-NOV-1999.

29-APR-1999; 99WO-CA000391.

29-APR-1998; 98CA-02230203.

(UYSH) UNIV SHERBROOKE.

Perreault J, Ananvoranich S, Lafontaine D;

WPI; 2000-096791/08.

New construction of nucleic acid enzyme useful for biotechnological,
diagnostic and therapeutic applications.

PT New construction of nucleic acid enzyme useful for biotechnological,
 PT diagnostic and therapeutic applications.
 PS Example 1; Page; 52pp; English.
 CC This is the nucleotide sequence of ribozyme deltaRzPl.2. This ribozyme
 CC cleaves substrate SP1.2 (see AA257634). The invention relates to a
 CC nucleic acid enzyme (e.g. deltaRzPl.2) that is constructed to have a
 CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
 CC substrate of the enzyme has the sequence 5'-H'-GNNHNN-3'. The binding
 CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
 CC cleavage site of the substrate (cleavage site is represented by *). At
 CC least one nucleotide is present 5' to the cleavage site of the substrate
 CC sequence. The enzyme of the invention is used to cleave a substrate
 CC nucleotide sequence at a specific cleavage site by mixing the substrate
 CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
 CC for example an inherited disease. The enzymes also have other
 CC therapeutic, biotechnological and diagnostic applications. Note: This
 CC sequence is not shown in the specification, but has been derived from the
 CC deltaRzPl.1 sequence (AA257636) shown in figure 1
 XX
 SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match 90.0%; Score 18; DB 3; Length 57;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CGCAUGGCUAAGGACCC 20
 Db 40 CGCAUGGCUAAGGACCC 57

RESULT 4
 AA257638
 ID AA257638 standard; RNA; 57 BP.
 XX
 AC AA257638;
 XX
 DT 15-SEP-2003 (revised)
 DT 05-APR-2000 (first entry)
 XX
 XX Trans-acting antigenomic delta ribozyme nucleotide sequence.
 XX
 XX Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
 XX inherited disease; ss.
 XX Hepatitis D virus.
 XX
 FH Key Location/Qualifiers
 FT misc_binding 1..6
 FT /*tag= a
 FT /note= "Forms double stranded region with bases 52-57"
 FT
 FT stem_loop 7..19
 FT /*tag= b
 FT misc_binding 20..25
 FT /*tag= c
 FT stem_loop 30..45
 FT /bound moiety= "SP1.1 substrate bases (AA257641) 5-11"
 FT /*tag= d
 FT misc_binding 52..57
 FT /*tag= e
 FT /note= "Forms a double stranded region with bases 6-11"
 FT
 FT WO9955856-A2.
 XX
 XX
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-CA000391.
 XX
 PR 29-APR-1998; 98CA-02230203.
 XX
 XX (UYSH) UNIV SHERBROOKE.
 PA
 XX

PI Perreault J, Ananvoranich S, Lafontaine D;
 XX WPI; 2000-096791/08.
 DR
 XX
 XX New construction of nucleic acid enzyme useful for biotechnological,
 PT diagnostic and therapeutic applications.
 PT
 XX Example 1; Fig 2; 52pp; English.
 PS
 XX This is the nucleotide sequence of a trans-acting antigenomic delta
 CC ribozyme of the invention. This ribozyme cleaves substrate SP1.1 (see
 CC AA257641). The invention relates to a nucleic acid enzyme (e.g.
 CC deltaRzPl.1) that is constructed to have a substrate binding portion with
 CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
 CC sequence 5'-H'-GNNHNN-3'. The binding portion of the enzyme (ribozyme)
 CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
 CC (cleavage site is represented by *). At least one nucleotide is present
 CC 5' to the cleavage site of the substrate sequence. The enzyme of the
 CC invention is used to cleave a substrate nucleotide sequence at a specific
 CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
 CC to cleave viral RNA or RNA causing for example an inherited disease. The
 CC enzymes also have other therapeutic, biotechnological and diagnostic
 CC applications. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 3; Length 57;
 Best Local Similarity 94.7%; Pred. No. 29;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCAUGGCUAAGGACCC 20
 Db 39 GCGCAUGGCUAAGGACCC 57

RESULT 5
 AA81564/c
 ID AA81564 standard; DNA; 11715 BP.
 XX
 AC AA81564;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-DEC-1990 (first entry)
 XX
 DE Genomic sequence encoding protein C.
 XX Human protein C; blood coagulation disorders; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT exon 2131..2200
 FT /*tag= a
 FT /label= exon I
 FT exon 3464..3630
 FT /*tag= b
 FT /label= exon II
 FT exon 5093..5117
 FT /*tag= c
 FT /label= exon III
 FT exon 5212..5349
 FT /*tag= d
 FT /label= exon IV
 FT exon 5452..5586
 FT /*tag= e
 FT /label= exon VI
 FT exon 8255..8397
 FT /*tag= f
 FT /label= exon VII
 FT exon 9270..9387
 FT /*tag= g
 FT /label= exon VIII
 FT exon 10517..12006

```

FT FT      /tag= h
XX FT      /label= exon IX
PN EP266190-A.
XX 04-MAY-1988.
PD
PF 28-OCT-1987; 87EP-00309528.
XX
PR 29-OCT-1986; 86US-00924462.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Foster DC, Murray MJ, Berkner KL;
XX
DR WPI; 1988-121259/18.
DR P-PSDB; AAP81205.
XX
XX Protein C DNA coding sequence and expression vector for prodn. - used for
PT treating blood coagulation disorders.
PT
XX Disclosure; Page ?; 35pp; English.
XX
CC In the construction of the full length protein C gene this sequence the
CC introns removed then is joined to a cDNA clone. The desired genomic:cDNA
CC is then generated by looping out of unwanted sequences using
CC oligonucleotide-directed deletion mutagenesis. The protein produced upon
CC transformation of mammalian host cells, contg. the recombinant DNA, has
CC substantially the same biological activity as natural protein C and is
CC hence useful in the treatment of blood coagulation disorders. See also
CC AAN81563. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 11715 BP; 2443 A; 3292 C; 3375 G; 2605 T; 0 U; 0 Other;

Query Match      87.0%; Score 17.4; DB 1; Length 11715;
Best Local Similarity 89.5%; Pred.No. 56;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGGACC 19
Db 877 GCGCATGGCAAGGGACC 859

RESULT 6
AAN70102/c
ID AAN70102 standard; DNA; 11724 BP.
XX
AC AAN70102;
XX
XX 25-MAR-2003 (revised)
DT 10-MAY-1991 (first entry)
XX
XX Complete genomic sequence of human Protein C.
DE
XX human Protein C; anti-coagulant; thrombosis; serine protease; ss.
KW
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT exon 2131..2200
FT /tag= a
FT /number= 1
FT /note="encodes amino acids -42 to -20"
FT intron 2201..3463
FT /tag= b
FT /number= 1
FT exon 2464..3630
FT /tag= c
FT /number= 2
FT /note="encodes amino acids -19 to +37"
FT intron 3631..5092
FT /tag= d
FT /number= 2

```

```

FT exon 5093..5117
FT /tag= e
FT /number= 3
FT /note="encodes amino acids 38 to 45"
FT intron 5118..5209
FT /tag= f
FT /number= 3
FT exon 5210..5347
FT /tag= g
FT /number= 4
FT /note="encodes amino acids 46 to 91"
FT intron 5348..5449
FT /tag= h
FT /number= 4
FT exon 5450..5584
FT /tag= i
FT /number= 5
FT /note="encodes amino acids 92 to 136"
FT intron 5585..8252
FT /tag= j
FT /number= 5
FT exon 8253..8395
FT /tag= k
FT /number= 6
FT /note="encodes amino acids 137 to 184"
FT intron 8396..9267
FT /tag= l
FT /number= 6
FT exon 9268..9385
FT /tag= m
FT /number= 7
FT /note="encodes amino acids 185 to 223"
FT intron 9386..10514
FT /tag= n
FT /number= 7
FT exon 10515..11104
FT /tag= o
FT /number= 8
FT /note="encodes amino acids 224 to 419"
FT polyA_signal 11151..11156
FT /tag= q
FT polyA_site 11173
FT /tag= r
FT polyA_signal 11380..11385
FT /tag= s
FT polyA_site 11399
FT /tag= t
XX
XX EP215548-A.
XX
XX 25-MAR-1987.
PD
XX
XX 26-JUN-1986; 86EP-00304970.
XX
XX 27-JUN-1985; 85US-00749600.
PR
XX 15-AUG-1985; 85US-00766109.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA (UNIW ) UNIV WASHINGTON.
XX
XX Murray MJ, Berkner KL, Foster DC, Davie EW;
XX
XX WPI; 1987-081505/12.
DR P-PSDB; AAP70855.
XX
XX Human protein C or activated protein C - prepd. using expression vector
XX capable of integration in mammalian host cell DNA.
XX
XX Claim 2; Page 33; 52pp; English.
XX
XX A lambda gt cDNA library was prepared from human liver mRNA. The library
XX was screened with iodine-125 labelled antibody to human protein C. A cDNA
XX which lacked the coding sequence for the pre-pro peptide and the forst 23
CC

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CC amino acids of protein C was isolated and used as a hybridisation probe.
CC The remainder of the coding sequence was obtained from a human genomic
CC DNA library in lambda Charon 4A. Recombinantly produced protein C can be
CC used to treat thrombotic disorders such as venous thrombosis. (Updated on
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 11724 BP; 2445 A; 3302 C; 3370 G; 2607 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 1; Length 11724;

Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGGACC 19
|||||:|||||
Db 877 GGCGCATGGCAAGGGACC 859

RESULT 7

AAH57497/c
ID AAH57497 standard; cDNA; 11724 BP.

XX AC AAH57497;

DT 10-SEP-2001 (first entry)

XX Human liver cell specific cDNA sequence SEQ ID NO:337.

XX Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX Homo sapiens.

OS WO200132927-A2.

XX 10-MAY-2001.

XX 02-NOV-2000; 2000WO-US030396.

PR 04-NOV-1999; 99US-0163508P.

XX (INCY-) INCYTE GENOMICS INC.

XX Sornasse T, Seilhamer JJ, Watson GA;

XX WPI; 2001-291057/30.

XX New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.

XX Claim 1; Page 254-257; 327pp; English.

XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by them are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology

SQ Sequence 11724 BP; 2443 A; 3298 C; 3375 G; 2608 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 4; Length 11724;

Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGGACC 19
|||||:|||||
Db 877 GGCGCATGGCAAGGGACC 859

RESULT 8

AAH32796/c
ID AAT32796 standard; DNA; 11725 BP.

XX AC AAT32796;

DT 25-MAR-2003 (revised)

DT 05-NOV-1996 (first entry)

XX Human protein C gene.

XX Activated protein C; serine protease; thrombosis; thrombolytic;
KW fibrinolytic; antithrombotic; blood clotting; therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1. .2250
FT /tag= a
FT /codon_start= 2131. .2133
FT intron 2251. .3463
FT /tag= b
FT exon 3464. .3630
FT /tag= c
FT intron 3631. .5092
FT /tag= d
FT exon 5093. .5117
FT /tag= e
FT intron 5118. .5209
FT /tag= f
FT exon 5210. .5347
FT /tag= g
FT intron 5348. .5449
FT /tag= h
FT exon 5450. .5583
FT /tag= i
FT intron 5583. .8252
FT /tag= j
FT exon 8253. .8395
FT /tag= k
FT intron 8395. .9268
FT /tag= l
FT misc_difference 9268
FT /tag= m
FT /note= "base 9268 is given as 'y' in the specification"
FT exon 9269. .9386
FT /tag= n
FT intron 9387. .10515
FT /tag= o
FT exon 10516. .11725
FT /tag= p
FT polyA_signal 11152. .11157
FT /tag= q
FT polyA_signal 11381. .11386
FT /tag= r

XX US5516650-A.

XX 14-MAY-1996.

XX 08-APR-1994; 94US-00225253.

PR 27-JUN-1985; 85US-00749600.

PR 29-OCT-1986; 86US-00924462.

PR 08-DEC-1987; 87US-00130370.

```
PR 28-FEB-1989; 89US-00317205.
PR 10-SEP-1990; 90US-00582131.
PR 04-DEC-1992; 92US-00987532.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Murray MJ, Berkner KL, Foster DC;
XX
XX WPI; 1996-251006/25.
XX P-PSDB; AAW02600.
XX
XX New DNA encoding modified forms of opt. activated protein C - and related
XX transformed cells for prodn. of recombinant protein C for use e.g. as an
XX anti-thrombotic agent.
XX
XX Example 1; Fig 4A-D; 34pp; English.
XX
XX A genomic DNA fragment (AAT32796) codes for human full-length protein C
XX (AAW02600), a zymogen of a serine protease that plays an important role
XX in blood clotting and in the generation of fibrinolytic activity in vivo.
XX It was obtd. from a human genomic library in phage Charon 4A using a
XX partial cDNA clone as probe. A complete cDNA clone (AAT32795) was also
XX produced. Protein C-encoding nucleic acids can be used for large-scale
XX prodn. of protein C, or variants modified to improve cleavage between the
XX heavy and light chains of the circulating intermediate. (Updated on 25-
XX MAR-2003 to correct PF field.)
XX
XX Sequence 11725 BP; 2444 A; 3295 C; 3372 G; 2613 T; 0 U; 1 Other;
SQ
Query Match 87.0%; Score 17.4; DB 2; Length 11725;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGCGCAUGCUGAAGGACC 19
Db 877 GGCGCATGCGCAAGGACC 859
RESULT 9
AAT79723/c
ID AAT79723 standard; DNA; 11725 BP.
XX
XX AAT79723;
AC
XX
XX 11-DEC-1997 (first entry)
DT
XX
XX Human protein C gene.
DE
XX
XX Protein C; transgenic animal; sheep; rabbit; cattle; goat; milk;
XX blood clotting; anticoagulant; human; ds.
XX
XX Homo sapiens.
FH
XX Key Location/Qualifiers
FT exon 3520..3630
FT /tag= a
FT intron 3631..5092
FT /tag= b
FT exon 5093..5117
FT /tag= c
FT intron 5118..5209
FT /tag= d
FT exon 5210..5347
FT /tag= e
FT intron 5348..5449
FT /tag= f
FT exon 5450..5584
FT /tag= g
FT intron 5585..8252
FT /tag= h
FT exon 8253..8395
FT /tag= i
FT intron 8396..9268
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FT /tag= j
FT 9269..9386
FT /tag= k
FT intron 9387..10515
FT /tag= l
FT exon 10516..11102
FT /tag= m
XX
XX WO9720043-A1.
XX
XX 05-JUN-1997.
XX
XX 26-NOV-1996; 96WO-US018866.
XX
XX 30-NOV-1995; 95US-00565074.
XX 13-JUN-1996; 96US-0019692P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX (PPLT-) PPL THERAPEUTICS.
XX
XX Garner I, Cottingham I, Temperley SM, Foster DC, Sprecher CA;
XX Prunkard DE;
XX
XX WPI; 1997-310599/28.
XX P-PSDB; AAW25086.
XX
XX Production of protein C in transgenic animal - useful for high quantity
XX protein C production with therapeutic value.
XX
XX Claim 6; Page 49-58; 99pp; English.
XX
XX This DNA sequence comprises human genomic DNA encoding protein C
XX (AAW25086). A claimed method for producing human protein C in the milk of
XX a transgenic animal involves: (a) providing a DNA construct comprising
XX DNA encoding a secretion signal and a protein C propeptide, operably
XX linked to DNA encoding two chain cleavage site-modified protein C, the 2
XX DNA sequences being linked to elements required for protein C expression
XX in a mammary gland of a host female animal, esp. the beta-lactoglobulin
XX gene promoter (see AAT79725); and (b) using the DNA construct to breed a
XX transgenic animal (esp. sheep, rabbit, cattle, goat) that produces
XX protein C in its milk, at least 90% of the protein C being in the two-
XX chain form. Modification of the protein C two-chain cleavage site (see
XX AAW25085) improves the maturation of recombinant protein C from single
XX chain to two-chain form. Also claimed is a non-human mammalian embryo
XX containing in its nucleus a heterologous DNA segment encoding cleavage
XX site-modified protein C
XX
XX Sequence 11725 BP; 2444 A; 3298 C; 3375 G; 2608 T; 0 U; 0 Other;
SQ
Query Match 87.0%; Score 17.4; DB 2; Length 11725;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGCGCAUGCUGAAGGACC 19
Db 877 GGCGCATGCGCAAGGACC 859
RESULT 10
AAZ32179/c
ID AAZ32179 standard; cDNA; 11725 BP.
XX
XX AAZ32179;
AC
XX
XX 13-JAN-2000 (first entry)
DT
XX
XX Human protein C nucleotide sequence.
XX
XX Human; coding sequence polymorphism; vascular pathology gene;
XX polymorphic site; phenotype correlation; forensic; paternity testing;
XX medicine; genetic analysis; vascular disease; ds.
XX
XX Homo sapiens.
OS
```

XX WO9950454-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99WO-US006473.
 XX
 PR 01-APR-1998; 98US-00054272.
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 XX Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
 PI WPI; 1999-620086/53.
 XX P-PSDB; AAY49560.
 DR
 DR
 XX
 PT Determination of polymorphisms in genes, especially those identifying
 PT predisposition to vascular disease.
 XX
 PS Claim 1; Fig 23; 134pp; English.
 XX
 CC AA232159 to AA232194 represent reference alleles for specifically claimed
 CC nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected from
 CC 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic analysis.
 CC AA49550 to AA49573 represent the proteins which correspond to some of
 CC the reference alleles
 XX
 SQ Sequence 11725 BP; 2444 A; 3298 C; 3375 G; 2608 T; 0 U; 0 Other;
 Query Match 87.0%; Score 17.4; DB 2; Length 11725;
 Best Local Similarity 89.5%; Pred. No. 56;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGCGCAUGGCUAAGGGACC 19
 |||||:|||||
 DB 877 GGCGCATGGCAAGGGACC 859
 RESULT 11
 AAF54051/c
 ID AAF54051 standard; cDNA; 11725 BP.
 XX
 AC AAF54051;
 XX
 DT 30-MAR-2001 (first entry)
 DE Human protein C cDNA, SEQ ID NO:50.
 XX
 KW Age-related gene regulation; gene expression; human protein C; hPC;
 KW 5' UTR; 5' untranslated region; age-regulatable expression construct;
 KW PEA-3 element; polyoma virus activator 3; antisense therapy;
 KW gene therapy; thrombosis; cardiovascular disease; diabetes;
 KW Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
 KW osteoarthritis; dementia; ss.
 XX
 OS Homo sapiens.
 PN WO200075279-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 06-JUN-2000; 2000WO-US015728.
 XX
 PR 09-JUN-1999; 99US-00328925.
 XX
 XX (UNMI) UNIV MICHIGAN.
 PA
 XX

PI Kurachi K, Kurachi S;
 XX WPI; 2001-061708/07.
 XX
 PT New regulatory elements that control age-related gene expression, useful
 PT in gene therapy and for reducing Factor IX expression.
 XX
 PS Disclosure; Fig 12; 225pp; English.
 XX
 CC The invention relates to nucleic acid sequences which regulate gene
 CC expression in an age-related manner and/or in a liver-specific manner.
 CC The invention identifies regions of the human factor IX (hFIX) gene, and
 CC a region of the human protein C (hPC) gene, which are age-related
 CC regulatory sequences. The hFIX age-related regulatory sequences are
 CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
 CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-
 CC 35655 of AAF54018) respectively. These elements act synergistically to
 CC increase hFIX levels over the lifespan of an individual; however, they
 CC can independently exert effects on hFIX mRNA in an age-related manner,
 CC with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
 CC mRNA levels, over time. AE5' also directs liver-specific expression. The
 CC hPC gene age-related regulatory sequence is found in the 5' UTR
 CC (AAF54081) and contains two PEA-3 (polyoma virus activator 3) elements
 CC (5'-GAGGAAA-3' and 5'-CAGGAG-3'). The age-related regulatory sequences of
 CC the invention, along with their homologues, variants and fragments, may
 CC be used in the construction of recombinant expression vectors for the
 CC expression of a desired sequence in an age-related fashion in a host
 CC cell. Preferred target genes for expression in such age-regulatable
 CC expression vectors include those encoding proteins involved in blood
 CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
 CC anti-coagulants protein C and antithrombin III), human alpha-1-
 CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
 CC Preferred promoters for use in such age-regulatable expression vectors
 CC include the human factor IX promoter, the T7 promoter, the T3 promoter
 CC and the SP6 promoter. The expression vectors of the invention may be used
 CC in gene therapy to provide age- related and/or liver-specific expression
 CC of target genes. Age-regulatable constructs may be used in the treatment
 CC of such age-related conditions such as thrombosis, cardiovascular
 CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
 CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
 CC to express factor IX antisense mRNA in the treatment of thrombotic
 CC conditions associated with the natural age-related rise in factor IX
 CC expression. Transgenic cells or animals that contain vectors of the
 CC invention are useful as models of these diseases, in screening for
 CC potential therapeutic agents and for studying normal processes such as
 CC ageing and gene expression. Fragments and homologues of age-related
 CC regulatory sequences, are useful as probes to detect, isolate or identify
 CC other such sequences in samples. The present sequence represents cDNA
 CC encoding hPC
 XX
 SQ Sequence 11725 BP; 2444 A; 3298 C; 3375 G; 2608 T; 0 U; 0 Other;
 Query Match 87.0%; Score 17.4; DB 4; Length 11725;
 Best Local Similarity 89.5%; Pred. No. 56;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGCGCAUGGCUAAGGGACC 19
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 DB 877 GGCGCATGGCAAGGGACC 859
 RESULT 12
 AAL56352/c
 ID AAL56352 standard; DNA; 13870 BP.
 XX
 AC AAL56352;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human protein C gene.
 XX
 KW Human; protein C; single nucleotide polymorphism; SNP; inflammation;
 KW gene; da.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT allele replace(1386,C)
FT FT /*tag= a
FT FT allele replace(2405,C)
FT FT /*tag= b
FT FT allele replace(2418,G)
FT FT /*tag= c
FT FT allele replace(2583,T)
FT FT /*tag= d
FT FT allele replace(3920,C)
FT FT /*tag= e
FT FT allele replace(4800,C)
FT FT /*tag= f
FT FT allele replace(4919,G)
FT FT /*tag= g
FT FT allele replace(4956,C)
FT FT /*tag= h
FT FT allele replace(5867,G)
FT FT /*tag= i
FT FT allele replace(6187,T)
FT FT /*tag= j
FT FT allele replace(9534,C)
FT FT /*tag= k
FT FT allele replace(12109,C)
FT FT /*tag= l
XX PN W02003100090-A2.
XX PD 04-DEC-2003.
XX PF 28-MAY-2003; 2003MO-CA000751.
XX PR 28-MAY-2002; 2002US-0383128P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Russell JA, Walley KR;
XX WPI; 2004-035164/03.
XX DR
XX PT Obtaining a prognosis for a patient having or at risk of developing an
XX PT inflammatory condition, e.g. systemic inflammatory response syndrome by
XX PT determining protein C polymorphism.
XX PS Claim 2; Page 15-20; Opp; English.
XX CC The present invention relates to a method of obtaining a prognosis for a
XX CC patient having or at risk of developing an inflammatory condition, which
XX CC comprises determining a genotype including one or more polymorphism sites
XX CC in the protein C gene for the patient, where the genotype is indicative
XX CC of an ability of the patient to recover from an inflammatory condition.
XX CC The method is useful in obtaining a prognosis for a patient having or at
XX CC risk of developing an inflammatory condition. Inflammatory condition is
XX CC selected from sepsis, septicemia, pneumonia, septic shock, Acute
XX CC Respiratory Distress Syndrome (ARDS), acute lung injury, infection,
XX CC pancreatitis, bacteraemia, peritonitis, abdominal, abscess, inflammation
XX CC due to trauma or surgery, chronic inflammatory disease, ischaemia,
XX CC ischaemia-perfusion injury of an organ or tissue, tissue damage due to
XX CC chemotherapy or radiotherapy and reactions to ingested, inhaled, infused,
XX CC injected or delivered substances, preferably systemic inflammatory
XX CC response syndrome (SIRS). The present sequence is the human protein C
XX CC gene
XX SQ Sequence 13870 BP; 2883 A; 3910 C; 4002 G; 3075 T; 0 U; 0 Other;
Query Match 87.0%; Score 17.4; DB 12; Length 13870;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCGCAUGGCUAAGGGACC 19

DB 2805 GGCGCATGGCAAGGGACC 2787
RESULT 13
ADN33950
ID ADN33950 standard; cDNA; 20188 BP.
XX AC ADN33950;
XX DT 17-JUN-2004 (first entry)
XX DE Human cDNA encoding NOV7a.
XX KW Human; ss; NOVX; pancreatic polypeptide; angiotensin; interleukin-1;
KW endothelin-2; endozepine; amphyresulin; metalloproteinase;
KW metabolic disorder; diabetes; obesity; infectious disease; anorexia;
KW cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic disturbance;
KW metabolic syndrome X; wasting disorder; antibacterial agent.
XX OS Homo sapiens.
XX PN US2004038230-A1.
XX PD 26-FEB-2004.
XX PF 04-NOV-2002; 2002US-00287190.
XX PR 05-NOV-2001; 2001US-0338626P.
XX PR 28-NOV-2001; 2001US-00996015.
XX PR 28-NOV-2001; 2001US-033912P.
XX PR 29-NOV-2001; 2001US-0334300P.
XX PR 03-DEC-2001; 2001US-0338198P.
XX PR 19-APR-2002; 2002US-0373806P.
XX PR 16-MAY-2002; 2002US-0381043P.
XX PR 07-AUG-2002; 2002US-0401593P.
XX PA (ALSO/) ALSOBROOK J P.
XX PA (ANDE/) ANDERSON D W.
XX PA (BOLD/) BOLDOG F L.
XX PA (BURG/) BURGESS C E.
XX PA (CHAN/) CHANT J S.
XX PA (CHAP/) CHAPOVAL A.
XX PA (CHAU/) CHAUDHURI A.
XX PA (EDIN/) EDINGER S R.
XX PA (EISE/) EISEN A.
XX PA (GANG/) GANGOLLI E A.
XX PA (GERL/) GERLACH V.
XX PA (GUOX/) GUO X S.
XX PA (JIWU/) JI W.
XX PA (KHRA/) KHRAMTSOV N V.
XX PA (LEIT/) LEITE M W.
XX PA (LILL/) LI L.
XX PA (MEZE/) MEZES P S.
XX PA (MILL/) MILLET I.
XX PA (OOIC/) OOI C E.
XX PA (ORTT/) ORT T.
XX PA (PADI/) PADIGARU M.
XX PA (PATT/) PATTURAJAN M.
XX PA (PENA/) PENA C E A.
XX PA (RAST/) RASTELLI L.
XX PA (RIEG/) RIEGER D K.
XX PA (SENG/) SENG K E Q.
XX PA (SMIT/) SMITHSON G.
XX PA (SPAD/) SPADERNA S K.
XX PA (SPYT/) SPYTEK K A.
XX PA (STON/) STONE D J.
XX PA (TWOI/) TWONLOW N.
XX PA (VERN/) VERNET C A M.
XX PA (VOSS/) VOSS E Z.
XX PA (ZERH/) ZERHUSEN B D.

(ZHON/) ZHONG M.

PA Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;
 XX Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;
 PI Gerlach V, Guo XS, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;
 PI Millet I, Ooi CE, Ort T, Padigar M, Patturajan M, Pena CEA;
 PI Rastelli L, Rieger DK, Senger KE, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;
 PI Zhong M;
 XX WPI: 2004-213932/20.
 DR P-PSDB; ADN33951.
 DR
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 PS Claim 20; SEQ ID NO 167; 129pp; English.
 XX The invention relates to 87 isolated NOVX polypeptides (NOV1-NOV85), their
 CC mature forms and their encoding polynucleotides having sequence
 CC similarity to pancreatic polypeptide (NOV1), angiotensin (NOV2),
 CC interleukin-1 (NOV3), endothelin-2 (NOV4), endozepine (NOV5),
 CC amphiregulin (NOV6) and metalloproteinase (NOV7). Also included the
 CC use of NOVX in the manufacture of a medicament for treating a human
 CC disease associated with NOVX, detecting NOVX in a sample via an
 CC immunoassay, identifying an agent that binds to the NOVX polypeptide,
 CC modulating the activity of NOVX, a vector comprising NOVX polynucleotide,
 CC a cell comprising the vector, an antibody that immunospecifically binds
 CC to NOVX, detecting the polynucleotide in a sample using a hybridisation
 CC assay; and producing the polypeptide comprising culturing the cell under
 CC conditions that lead to expression of the polypeptide. NOVX and its
 CC polynucleotide are used to prevent, diagnose or treat a medical condition
 CC in human related to the aberrant expression and activity of NOVX
 CC polypeptides e.g. metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. NOVX may also be used as
 CC an antigen in the production of antibodies and in assays to identify
 CC modulators (agonists and antagonists) of the expression and activity of
 CC NOVX. The present sequence encodes a NOVX protein.
 XX
 SQ Sequence 20188 BP; 4653 A; 5404 C; 5682 G; 4428 T; 0 U; 21 Other;
 Query Match 85.0%; Score 17; DB 12; Length 20188;
 Best Local Similarity 88.2%; Pred. No. 96;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GGCGCAUGGCUAAGGGA 17
 DB 20057 GGCGCATGCTAAGGGA 20073
 RESULT 14
 AD7C1539
 ID AD7C1539 standard; cDNA; 20190 BP.
 XX
 AC AD7C1539;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human NOV7a encoding cDNA SEQ ID NO:167.
 XX human; NOVX; cytostatic; anorectic; antidiabetic; antiparkinsonian;
 KW neuroprotective; nootropic; immunomodulator; antiarteriosclerotic;
 KW nephrotropic; osteopathic; vaccine; gene therapy; cancer; obesity;
 KW diabetes; metabolic disorder; anorexia; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; immune disorder;
 KW haematopoietic disorder; atherosclerosis; renal failure; hyperkalaemia;
 KW hypoglycaemia; bone disorder; wasting disorder; gene; ss.

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 1..2205
 FT /*tag= a
 FT /product= "NOV7a"
 XX
 PN WO2003040329-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 05-NOV-2002; 2002WO-US035535.
 XX
 XX 05-NOV-2001; 2001US-0338626P.
 PR 28-NOV-2001; 2001US-0096015.
 PR 28-NOV-2001; 2001US-0333912P.
 PR 29-NOV-2001; 2001US-0334300P.
 PR 03-DEC-2001; 2001US-0338196P.
 PR 19-APR-2002; 2002US-0373806P.
 PR 16-MAY-2002; 2002US-0381043P.
 PR 07-AUG-2002; 2002US-0401593P.
 PR 04-NOV-2002; 2002US-00287190.
 XX (CURA-) CURAGEN CORP.
 PA
 XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;
 PI Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;
 PI Gerlach VL, Guo X, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;
 PI Millet I, Ooi CE, Ort T, Padigar M, Patturajan M, Pena CEA;
 PI Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;
 PI Zhong M;
 XX WPI: 2003-441554/41.
 DR P-PSDB; ADC71540.
 DR
 XX New NOVX polypeptides and nucleic acids for diagnosing, preventing or
 PT treating NOVX-associated disorders, e.g. cancer, obesity, diabetes or
 PT atherosclerosis, and for chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 20; SEQ ID NO 167; 112pp; English.
 XX
 CC The present invention describes novel human proteins designated NOVX,
 CC where X can be an integer of 1 to 7. The NOVX protein and nucleotide
 CC sequences have cytostatic, anorectic, antidiabetic, antiparkinsonian,
 CC neuroprotective, nootropic, immunomodulator, antiarteriosclerotic,
 CC nephrotropic and osteopathic activities, and can be used in vaccines and
 CC in gene therapy. The NOVX proteins can be used in manufacturing a
 CC medicament for treating a syndrome associated with a human disease, the
 CC disease selected from a pathology associated with the protein. The
 CC disease can be cancer. NOVX proteins, nucleic acid molecules and
 CC antibodies may also be used for diagnosing, treating or preventing other
 CC pathologies associated with aberrant NOVX expression or activity, such as
 CC obesity, diabetes, metabolic disorders, anorexia, neurodegenerative
 CC diseases (e.g. Parkinson's disease or Alzheimer's disease), immune
 CC disorders, haematopoietic disorders, atherosclerosis, renal failure,
 CC hyperkalaemia, hypoglycaemia, bone disorders and wasting disorders. The
 CC NOVX nucleic acids and proteins may also be used in chromosome mapping,
 CC tissue typing, predictive medicine and pharmacogenomics. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 20190 BP; 4650 A; 5340 C; 5756 G; 4429 T; 0 U; 15 Other;
 Query Match 85.0%; Score 17; DB 10; Length 20190;
 Best Local Similarity 88.2%; Pred. No. 96;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GGCGCAUGGCUAAGGGA 17
 DB 20059 GGCGCATGCTAAGGGA 20075

RESULT 15
ADQ19501/c
ID ADQ19501 standard; DNA; 135005 BP.
XX
AC ADQ19501;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 2320; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytotstatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 135005 BP; 32951 A; 33605 C; 32661 G; 35788 T; 0 U; 0 Other;
Query Match 85.0%; Score 17; DB 12; Length 135005;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGCGAUGGCUAAGGA 17
Db 108776 GCGCGATGGCTAAGGA 108760
Search completed: March 15, 2005, 11:20:20
Job time : 117.702 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:18:52 ; Search time 33.1579 Seconds
(without alignments)
986.961 Million cell updates/sec

Title: US-09-699-667E-64
Perfect score: 20
Sequence: 1 ggcgauggcuaaggagacc 20
Scoring table: IDENTITY NUCDX
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.4	87.0	601	US-09-949-016-18503	Sequence 18503, A
C 2	17.4	87.0	601	US-09-949-016-176107	Sequence 176107, A
C 3	17.4	87.0	11725	US-08-756-506-1	Sequence 1, Appl
C 4	17.4	87.0	11725	US-09-328-925-50	Sequence 50, Appl
C 5	17.4	87.0	11725	US-09-054-272-31	Sequence 31, Appl
C 6	17.4	87.0	14802	US-09-949-016-16753	Sequence 16753, A
C 7	15.8	79.0	1089	US-09-252-991A-14778	Sequence 14778, A
C 8	15.8	79.0	1482	US-09-252-991A-14656	Sequence 14656, A
C 9	15.4	77.0	3595	US-09-949-016-4833	Sequence 4833, Ap
10	15.4	77.0	25198	US-09-949-016-16575	Sequence 16575, A
11	15.2	76.0	601	US-09-949-016-148214	Sequence 148214, A
C 12	15.2	76.0	662	US-08-441-507-1	Sequence 1, Appl
C 13	15.2	76.0	662	US-07-969-875A-1	Sequence 1, Appl
C 14	15.2	76.0	663	US-09-902-540-7911	Sequence 7911, Ap
C 15	15.2	76.0	711	US-08-622-046B-2	Sequence 2, Appl
C 16	15.2	76.0	711	US-08-622-046B-13	Sequence 13, Appl
C 17	15.2	76.0	711	US-09-100-264-2	Sequence 2, Appl
C 18	15.2	76.0	711	US-08-843-076D-2	Sequence 2, Appl
C 19	15.2	76.0	760	US-08-768-859A-7	Sequence 7, Appl
C 20	15.2	76.0	760	US-08-767-820A-7	Sequence 7, Appl
C 21	15.2	76.0	760	PCT-US95-06157-7	Sequence 7, Appl
C 22	15.2	76.0	766	US-08-768-859A-9	Sequence 9, Appl
C 23	15.2	76.0	766	US-08-767-820A-9	Sequence 9, Appl
C 24	15.2	76.0	766	US-08-622-046B-6	Sequence 6, Appl
C 25	15.2	76.0	766	US-08-622-046B-17	Sequence 17, Appl
C 26	15.2	76.0	766	US-09-100-264-6	Sequence 6, Appl
C 27	15.2	76.0	766	US-08-843-076D-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-18503/c
; Sequence 18503, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18503
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-18503

Query Match 87.0%; Score 17.4; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 21;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACC 19
DB 523 GCGCGATGCAAGGACC 505
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|||||:|||||

RESULT 2

US-09-949-016-176107/c
; Sequence 176107, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

C 28 15.2 76.0 766 5 PCT-US95-06157-9 Sequence 9, Appli
C 29 15.2 76.0 822 3 US-09-100-264-8 Sequence 8, Appli
C 30 15.2 76.0 832 3 US-08-768-859A-5 Sequence 5, Appli
C 31 15.2 76.0 832 3 US-08-768-859A-20 Sequence 20, Appli
C 32 15.2 76.0 832 3 US-08-767-820A-5 Sequence 5, Appli
C 33 15.2 76.0 832 3 US-08-767-820A-20 Sequence 20, Appli
C 34 15.2 76.0 832 3 US-08-622-046B-4 Sequence 4, Appli
C 35 15.2 76.0 832 3 US-08-622-046B-15 Sequence 15, Appli
C 36 15.2 76.0 832 4 US-08-843-076D-4 Sequence 4, Appli
C 37 15.2 76.0 832 5 PCT-US95-06157-5 Sequence 5, Appli
C 38 15.2 76.0 1341 3 US-08-983-075D-6 Sequence 6, Appli
C 39 15.2 76.0 1358 3 US-08-983-075D-8 Sequence 8, Appli
C 40 15.2 76.0 1507 4 US-09-949-016-1840 Sequence 1840, Ap
C 41 15.2 76.0 3279 3 US-09-439-313-382 Sequence 382, App
C 42 15.2 76.0 3279 3 US-09-352-616A-382 Sequence 382, App
C 43 15.2 76.0 3279 4 US-09-636-215-382 Sequence 382, App
C 44 15.2 76.0 3279 4 US-09-685-166A-382 Sequence 382, App
C 45 15.2 76.0 3279 4 US-09-679-426-382 Sequence 382, App

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176107
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-176107

Query Match      87.0%; Score 17.4; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 21;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGCGCAUGGCUAAGGACC 19
Db      523 GGCGCATGCGCAAGGACC 505
|||||:|||||
;
RESULT 3
US-08-756-506-1/c
; Sequence 1, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Cottingham, Ian R.
; APPLICANT: Temperley, Simon M.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prunkard, Donna E.
; TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
; TITLE OF INVENTION: ANIMALS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,506
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 95-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(3520..3630, 5093..5117, 5210..5347, 5450
; LOCATION: ..5584, 8253..8395, 9269..9386, 10516..11102)
US-08-756-506-1

Query Match      87.0%; Score 17.4; DB 2; Length 11725;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGCGCAUGGCUAAGGACC 19
Db      523 GGCGCATGCGCAAGGACC 505
|||||:|||||
;
RESULT 4
US-09-328-925-50/c
; Sequence 50, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 11725
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-50

Query Match      87.0%; Score 17.4; DB 4; Length 11725;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGCGCAUGGCUAAGGACC 19
Db      877 GGCGCATGCGCAAGGACC 859
|||||:|||||
;
RESULT 5
US-09-054-272-31/c
; Sequence 31, Application US/09054272
; Patent No. 6692909
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George Q.
; APPLICANT: Carell, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Rozen, Steven G.
; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI98-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
;
QY      1 GGCGCAUGGCUAAGGACC 19
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; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-09-054-272-31

Query Match 87.0%; Score 17.4; DB 4; Length 11725;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGCGCAUGGCUAAGGGACC 19
|||||:|||||
DB 877 GGCGCATGGCAAGGGACC 859

RESULT 6

US-09-949-016-16753/c
; Sequence 16753, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16753
; LENGTH: 14802
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(14802)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16753

Query Match 87.0%; Score 17.4; DB 4; Length 14802;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGCGCAUGGCUAAGGGACC 19
|||||:|||||
DB 2247 GGCGCATGGCAAGGGACC 2229

RESULT 7

US-09-252-991A-14778/c
; Sequence 14778, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14778

; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (116)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-14778

Query Match 79.0%; Score 15.8; DB 4; Length 1089;
Best Local Similarity 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGCGCAUGGCUAAGGGACC 19
|||||:|||||
DB 189 GGCCCATGGCAAGGGACC 171

RESULT 8

US-09-252-991A-14656/c
; Sequence 14656, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14656
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-14656

Query Match 79.0%; Score 15.8; DB 4; Length 1482;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGCGCAUGGCUAAGGGACC 19
|||||:|||||
DB 136 GGCCCATGGCAAGGGACC 118

RESULT 9

US-09-949-016-4833
; Sequence 4833, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4833

```
; LENGTH: 3595
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4833

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 4; Length 3595;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACCC 20
Db 2520 GCATGGCTGAGGACCC 2536

RESULT 10
US-09-949-016-16575
; Sequence 16575, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16575
; LENGTH: 25198
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(25198)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16575

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 4; Length 25198;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUGGCUAAGGACCC 20
Db 22122 GCATGGCTGAGGACCC 22138

RESULT 11
US-09-949-016-148214
; Sequence 148214, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148214
; LENGTH: 601
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-148214

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 601;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACCC 20
Db 145 GCGCGAUGGCUAAGGACCC 164

RESULT 12
US-08-441-507-1/c
; Sequence 1, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; TITLE OF INVENTION: Dactylon
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy B.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..435
US-08-441-507-1

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 662;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACCC 20
Db 343 GCGCGATGCTGAAGGACCC 324

RESULT 13
US-07-969-875A-1/c
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; Sequence 1, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Singh, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..435
; US-07-969-875A-1

Query Match          76.0%; Score 15.2; DB 3; Length 662;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  GGCGCAUGGCUAAGGACCC 20
Db      343 GGCGGATGGTGAAGGACCC 324
      |||||:|||||
      |||||:|||||

RESULT 14
US-09-902-540-7911/c
; Sequence 7911, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7911
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
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```
US-09-902-540-7911

Query Match          76.0%; Score 15.2; DB 4; Length 663;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  GGCGCAUGGCUAAGGACCC 20
Db      94  GGCGGATGGCGAAGGACCC 75
      |||||:|||||
      |||||:|||||

RESULT 15
US-08-622-046B-2/c
; Sequence 2, Application US/08622046B
; Patent No. 6103237
; GENERAL INFORMATION:
; APPLICANT: Saedi, Mohammed S.
; APPLICANT: Mikolajczyk, Stephen D.
; TITLE OF INVENTION: Stable Variant HK2 Polypeptide
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/622,046B
; FILING DATE: 26-MARCH-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 476.001US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-373-6903
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-622-046B-2

Query Match          76.0%; Score 15.2; DB 3; Length 711;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  GGCGCAUGGCUAAGGACCC 20
Db      633 GGCACATGGCTCAGGGCCCC 614
      |||||:|||||
      |||||:|||||

Search completed: March 15, 2005, 15:26:39
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:06:47 ; Search time 868.86 Seconds
(without alignments)
876.189 Million cell updates/sec

Title: US-09-699-667E-64
Perfect score: 20
Sequence: 1 ggcgaaggcuaggagacc 20

Scoring table: IDENTITY_NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	87.0	519	8 BH090915	BH090915 RPCI-24-2
C 2	16.8	84.0	240	8 AZ844319	AZ844319 2M0143C17
C 3	16.8	84.0	394	2 BF884568	BF884568 CM2-ET019
C 4	16.8	84.0	468	7 H49655	H49655 YQ20h07.s1
C 5	16.8	84.0	471	8 BH101439	BH101439 RPCI-24-3
C 6	16.8	84.0	492	8 AZ901413	AZ901413 RPCI-24-1
C 7	16.8	84.0	514	8 AZ791672	AZ791672 2M0041L08
C 8	16.8	84.0	555	5 BP446790	BP446790 BP446790
C 9	16.8	84.0	557	1 A1233177	A1233177 EST229865
C 10	16.8	84.0	568	7 CN383794	CN383794 411714 B
C 11	16.8	84.0	597	2 BE885239	BE885239 601506306
C 12	16.8	84.0	634	7 CN369119	CN369119 170005999
C 13	16.8	84.0	709	9 CR277771	CR277771 Forward s10
C 14	16.8	84.0	757	4 B1329017	B1329017 602980410
C 15	16.8	84.0	825	6 CB961961	CB961961 AGENCOURT
C 16	16.8	84.0	826	6 CB961668	CB961668 AGENCOURT
C 17	16.8	84.0	899	2 BE619299	BE619299 601473181
C 18	16.8	84.0	931	5 BU856404	BU856404 AGENCOURT
C 19	16.8	84.0	953	5 BU846054	BU846054 AGENCOURT
C 20	16.8	84.0	1059	5 BQ070932	BQ070932 AGENCOURT
C 21	16.8	84.0	1165	8 BZ562536	BZ562536 pac82-164
C 22	16.4	82.0	557	4 EG023212	EG023212 d10c01.y
C 23	16.4	82.0	575	2 BF231936	BF231936 d10c01.x
C 24	16.4	82.0	589	7 CK428113	CK428113 laj10g07.

25	16.4	82.0	751	5 BX847762	BX847762 BX847762
26	16.4	82.0	767	4 BG069840	BG069840 H3080F11-
27	16.4	82.0	784	8 BZ137357	BZ137357 CH230-288
C 28	16.4	82.0	905	7 CN501110	CN501110 AGENCOURT
C 29	16.4	82.0	916	5 BU361862	BU361862 603789355
C 30	16.4	82.0	971	9 CC995546	CC995546 ZUAH125TV
C 31	16	80.0	623	7 CV432461	CV432461 RT0762 Ch
C 32	15.8	79.0	202	7 CO395649	CO395649 AGENCOURT
C 33	15.8	79.0	226	2 BM152189	BM152189 BB152189
C 34	15.8	79.0	261	4 BM602859	BM602859 170006870
C 35	15.8	79.0	291	2 AW878055	AW878055 MR3-OT000
C 36	15.8	79.0	384	6 BY626060	BY626060 BY626060
C 37	15.8	79.0	401	6 BY635564	BY635564 BY635564
C 38	15.8	79.0	415	5 BX619468	BX619468 BX619468
C 39	15.8	79.0	425	1 AA989300	AA989300 0808409.s
C 40	15.8	79.0	427	6 BY614776	BY614776 BY614776
C 41	15.8	79.0	437	5 BQ494421	BQ494421 EST03587
C 42	15.8	79.0	442	6 CD568026	CD568026 EST0262 R
C 43	15.8	79.0	451	6 CB787029	CB787029 AMGNNUC.M
C 44	15.8	79.0	451	8 AQ588920	AQ588920 C17B1-E1-
C 45	15.8	79.0	459	1 AJ455698	AJ455698 AJ455698

ALIGNMENTS

RESULT 1
BH090915/c 519 bp DNA linear GSS 18-JUL-2001
LOCUS
DEFINITION
RPCI-24-281E19.TV RPCI-24 Mus musculus genomic clone
RPCI-24-281E19, genomic survey sequence.
ACCESSION
BH090915
VERSION
BH090915.1 GI:14910820
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 519)
Zhang, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartabeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-281E19.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
Tel: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Plate: 281 row: E column: 19
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..519
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-281E19"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site1: BamHI; Site2: BamHI; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the

FEATURES source

BamHI sites using MboI partially digested male C57BL/6J DNA."

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 519;
 Best Local Similarity 84.2%; Pred. No. 5.8e+02;
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACCC 19
 |||||:||||:||||
 Db 127 GCGCGATGGCTAAGGAACC 109

RESULT 2

AZ844319/c
 LOCUS AZ844319 240 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0143C17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0143C17 R, genomic survey sequence.

ACCESSION AZ844319

VERSION AZ844319.1 GI:13014227

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 240)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islám, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

Plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0143 row: C column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 240.

Location/Qualifiers

FEATURES

source

1. .240
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0143C17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [GI4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 240;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACCC 20
 |||||:||||:||||
 Db 121 GCGCGATGGCTCAGGACCC 102

RESULT 3

BF884568/c
 LOCUS BF884568 394 bp mRNA linear EST 17-JAN-2001
 DEFINITION CM2-ET0193-261200-654-h08 ET0193 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF884568

VERSION BF884568.1 GI:12274717

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 394)

AUTHORS
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bais, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=CM2&t2=CM2-ET0193-
 261200-654-h08&t3=2000-12-26&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 384.

FEATURES

source

1. .394
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ET0193"
 /note="Organ: lung_tumor; Vector: puc18; Site: 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 394;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCGAUGGCUAAGGACCC 20
 |||||:||||:||||
 Db 179 GCGCGATGGCTTAGAGACCC 160

Chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."


```

RESULT 4
H49655/c
LOCUS
DEFINITION YQ20h07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:274428 3', mRNA sequence.
ACCESSION H49655
VERSION H49655.1 GI:989496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 468)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterson,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 955
High quality sequence stops: 345
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 955 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 345.
FEATURES
source
Location/Qualifiers
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3798235"
/db_xref="taxon:9606"
/clone="IMAGE:274428"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/notes="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAGAAATTAATAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
Query Match 84.0%; Score 16.8; DB 7; Length 468;
Best Local Similarity 80.0%; Pred.No.1.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGCGAUGGCUAAGGACCC 20
|||||:|||||
Db 380 GCGCGATGCTTAGAGACCC 161
|||||:|||||

RESULT 5
BH101439/c
LOCUS
DEFINITION RPCI-24-304P16.TJ RPCI-24 Mus musculus genomic clone
IMAGE:274304P16, genomic survey sequence.
ACCESSION BH101439
VERSION BH101439.1 GI:14926316
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 492)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-304P16.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 304 row: P column: 16
Seq primer: SP6
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..471
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-304P16"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/notes="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI; The
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."
ORIGIN
Query Match 84.0%; Score 16.8; DB 8; Length 471;
Best Local Similarity 80.0%; Pred.No.1.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGCGAUGGCUAAGGACCC 20
|||||:|||||
Db 415 GCGCGTGGCTAAGGACCC 396
|||||:|||||

RESULT 6
AZ901413
LOCUS
DEFINITION RPCI-24-154A19.TV RPCI-24 Mus musculus genomic clone
IMAGE:274154A19, genomic survey sequence.
ACCESSION AZ901413
VERSION AZ901413.1 GI:13220358
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 492)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-154A19.TJ

```

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end page: http://www.tigr.org/tcdb/bac_ends/mouse/bac_end_intro.html
Plate: 154 row: A column: 19
Seq primer: T7
Class: BAC ends.

FEATURES source

Location/Qualifiers
1. .492
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-154A19"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 492;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGACCC 20
|||:||||:|||||
Db 162 GGAGCATGGCTAAGGGAGCC 181

RESULT 7

AZ791672/c 514 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
2M004108R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M004108 R, genomic survey sequence.

ACCESSION
AZ791672
AZ791672.1 GI:129334808
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 514)
Islan,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0041 row: L column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

FEATURES source

High quality sequence stop: 514.
Location/Qualifiers
1. .514
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0041L08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 514;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGACCC 20
|||:||||:|||||
Db 322 GGGCATGGCTCAGGGACCC 303

RESULT 8

BP446790 555 bp mRNA linear EST 30-DEC-2003
LOCUS
DEFINITION
BP446790 full-length enriched swine cDNA library, adult liver Sus scrofa cDNA clone LVR010038G07 5', mRNA sequence.

ACCESSION
BP446790
BP446790.1 GI:40436857
EST.

KEYWORDS
Sus scrofa (pig)

ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
1 (bases 1 to 555)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.

TITLE
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries

JOURNAL
Nucleic Acids Res. 32 (1), D484-D488 (2004)

COMMENT
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319

```

FEATURES
  source
    Low quality bases were trimmed based on the quality values.
    Location/Qualifiers
      1..555
        /organism="Sus scrofa"
        /mol_type="mRNA"
        /db_xref="taxon:9823"
        /clone="LVR010038G07"
        /tissue_type="liver"
        /dev_stage="adult"
        /clone_lib="full-length enriched swine cDNA library, adult
        liver"
ORIGIN
  Query Match      84.0%; Score 16.8; DB 5; Length 555;
  Best Local Similarity 80.0%; Pred. No. 1.2e+03;
  Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGCGCAUGGCUAAGGACCC 20
Db 115 GCGCGCATGGCTTAGGGACG 134

RESULT 9
LOCUS AI233177
DEFINITION EST229865 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
RKICL81 3' end, mRNA sequence.
ACCESSION AI233177
VERSION AI233177.1 GI:3817057
KEYWORDS EST.
SOURCE Rattus sp.
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
    Rattus.
  1 (bases 1 to 557)
    Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
    Kerlavage,A.R. and Adams,M.D.
    Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
    Gene Index
  JOURNAL Unpublished (1998)
  COMMENT Contact: Lee, NH
    The Institute for Genomic Research
    9712, Medical Center Drive, Rockville, MD 20850, USA
    Tel: (301)-838-3529
    Fax: (301)-838-0208
    Email: nhlee@tigr.org
    Seq primer: M13-21.
    Location/Qualifiers
      1..557
        /organism="Rattus sp."
        /mol_type="mRNA"
        /db_xref="ATCC (inhost):2040225"
        /db_xref="taxon:10118"
        /clone="RKICL81"
        /clone_lib="Normalized rat kidney, Bento Soares"
        /notes="Organ: kidney; Vector: pTT3Pac; Site_1: EcoRI;
        Site_2: NotI"
ORIGIN
  Query Match      84.0%; Score 16.8; DB 1; Length 557;
  Best Local Similarity 80.0%; Pred. No. 1.2e+03;
  Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGCGCAUGGCUAAGGACCC 20
Db 286 GCGCGCATGGCTTAGGGACCC 305

RESULT 10
LOCUS CN383794
DEFINITION 4117714 BARC_3GAL chicken mixed tissue Gallus gallus cDNA clone

```

```

3GAL_13E17 5', mRNA sequence.
CN383794
VERSION CN383794.1 GI:53550640
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
    Phasianinae; Gallus.
  1 (bases 1 to 568)
    Matukumalli,L.K. and Van Tassel,C.P.
    EvoCk-Clover,C.M., Ashwell,C.M., McMurtry,J.P., Lillehoj,H.S.,
    Characterization of expressed sequence tags generated from multiple
    chicken tissues
  JOURNAL Unpublished (2004)
  COMMENT Contact: Christina M. Clover
    Growth Biology Laboratory
    Animal and Natural Resources Institute
    Bldg. 200 Rm215 BARC-East, Beltsville, MD 20705, USA
    Tel: 3015048224
    Fax: 3015048623
    Email: chrisc@anri.barc.usda.gov
    Single pass sequencing. Bases called and trimmed with phred
    0.00925 using options -trim_alt "-trim_fasta. Vector identified
    by cross_match using options -minmatch 12 -minscore 18
    Plate: 13 row: E column: 17
    Seq primer: CCCAGTCACGACGCTTGTAAACG
    High quality sequence stop: 568.
    Location/Qualifiers
      1..568
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /strain="Leghorn and broiler"
        /db_xref="taxon:9031"
        /clone="3GAL_13E17"
        /lab_host="DH5alpha"
        /clone_lib="BARC_3GAL chicken mixed tissue"
        /notes="Vector: pBluescript, SK+, Stratagene; Site 1: NotI;
        Site 2: EcoRI; Normalized library of pooled RNA isolated
        from whole brain, ultimobranchial gland, parathyroid
        gland, cecal tonsil and primordial germ cells Multiple"
ORIGIN
  Query Match      84.0%; Score 16.8; DB 7; Length 568;
  Best Local Similarity 80.0%; Pred. No. 1.2e+03;
  Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGCGCAUGGCUAAGGACCC 20
Db 504 GCGCGCATGGCTTAGGGACCC 523

RESULT 11
LOCUS BE885239/c
DEFINITION 601506306F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908089 5',
mRNA sequence.
ACCESSION BE885239
VERSION BE885239.1 GI:10334015
KEYWORDS EST.
SOURCE Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 597)
    NIH-MGC http://mgc.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: ATCC
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

```

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1A4W719 row: k column: 02
 High quality sequence stop: 420.
 Location/Qualifiers

FEATURES

1..597
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3908089"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 2.1 kb."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 597;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCACATGGCTTAGGGACCC 20
 |||||:||||:|||||
 Db 551 GGCACATGGCTTAGGGACCC 532

RESULT 12

LOCUS CN369119 634 bp mRNA linear EST 16-MAY-2004
 DEFINITION 1700059936909 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN369119
 VERSION CN369119.1 GI:47369053
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 634)
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Lebkowski, J and Stanton, L.W.

TITLE

Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation

JOURNAL

Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT

Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 634 Std Error: 0.00.

FEATURES

Location/Qualifiers
 1..634
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_lib="GRN_PRENEU"
 /note="Oligo dr primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic acid and mitogens."

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 634;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCACATGGCTTAGGGACCC 20
 |||||:||||:|||||
 Db 158 GGCACATGGCTTAGGGACCC 177

RESULT 13

CR277771/c

LOCUS

DEFINITION

Forward strand read from insert in 5'HPRT insertion targeting and
 chromosome engineering clone MHPN406h24, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

CR277771 709 bp DNA linear GSS 06-JUL-2004
 Forward strand read from insert in 5'HPRT insertion targeting and
 chromosome engineering clone MHPN406h24, genomic survey sequence.
 CR277771.1 GI:50056748
 GSS; genome survey sequence; MICER.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 709)
 Adams, D.J., Bliggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
 Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
 Rogers, J. and Bradley, A.

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

1..709

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="MHPN406h24"

/clone_lib="MHPN"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

0;

0;

0;

0;

0;

0;

0;

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0;

0;

0;

0;

0;

0;

0;

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5133243"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NCI_CGAP_L19"

/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 84.0%; Score 16.8; DB 4; Length 757;

Best Local Similarity 85.0%; Pred. No. 1.2e+03;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGACCC 20

|||||:|||||

|||:|||||

741 GGAGCAGGCTAAGGACCC 722

RESULT 15

CB961961

LOCUS

DEFINITION CB961961 825 bp mRNA linear EST 29-APR-2003

AGENCOURT_13665758 NIH_MGC_148 Homo sapiens cDNA clone

IMAGE:30349111 5', mRNA sequence.

CB961961

CB961961.1 GI:30218078

EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 825)

NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapps-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM392 row: o column: 08

High quality sequence stop: 582.

FEATURES

source

1..825

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30349111"

/tissue_type="pre-eclampsia placenta"

/lab_host="DH10B Tona"

/clone_lib="NIH MGC 148"

/note="Organ: Placenta; Vector: pBluescriptR; Site_1:

all-XhoI; Site_2: BamHI; Library is oligo-dT primed and

directionally cloned using primer

5'-TTTTTTTTTTTNN-3', size-selected for average insert

size 2.3 kb and normalized to RGT 5. This is a primary

library enriched for full-length clones and constructed

using the Cap-trapper method (Carninci, in preparation).

Library constructed by M. Brownstein (NHGRI, in preparation).

National Institutes of Health). Note: this is a NIH_MGC

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 825;

Best Local Similarity 80.0%; Pred. No. 1.2e+03;

Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGCAUGGCUAAGGACCC 20

|||||:|||||

|||:|||||

144 GGCGCATGGCTTAGGACGC 163

Search completed: March 15, 2005, 15:20:34

Job time : 875.86 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:20:59 ; Search time 1488.44 Seconds
(without alignments)
946.212 Million cell updates/sec

Title: US-09-699-667E-65

Perfect score: 37

Sequence: 1 ggguccaccuccgcggunnnmngggcaugcsby 37

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 241816

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23.8	64.3	55	1	AA232965
C 2	22.8	61.6	51	8	BH413716
C 3	22.6	61.1	50	1	AU104848
C 4	22.6	61.1	53	9	CR002872
C 5	22.6	61.1	58	9	CR101542
C 6	22.4	60.5	43	9	CG774833
C 7	22.4	60.5	49	7	H23825
C 8	21.8	58.9	43	8	AZ585629
C 9	21.8	58.9	45	4	BM395132
C 10	21.8	58.9	49	1	AA878748
C 11	21.6	58.4	53	9	CL214958
C 12	21.6	58.4	58	1	AI612870
C 13	21.2	57.3	49	1	AA993587
C 14	21.2	57.3	55	9	TA234D12P
C 15	21.2	57.3	57	9	CL234247
C 16	21	56.8	31	1	AI688077
C 17	21	56.8	56	2	AW063221
C 18	20.8	56.2	50	9	CR021509
C 19	20.8	56.2	57	9	TA348B10P
C 20	20.8	56.2	58	8	BH803980
C 21	20.6	55.7	41	8	AZ537682
C 22	20.6	55.7	57	5	BQ256702
C 23	20.6	55.7	60	1	AA762539
C 24	20.6	55.7	60	6	CD952940

25	20.4	55.1	34	1	AI584193
26	20.4	55.1	48	4	BI094799
27	20.4	55.1	50	1	AU104597
28	20.4	55.1	50	1	AU104642
29	20.4	55.1	50	1	AU104689
30	20.4	55.1	55	1	AA861787
C 31	20.4	55.1	55	6	CB214675
C 32	20.4	55.1	55	8	AZ458661
C 33	20.2	54.6	41	9	CL791728
C 34	20.2	54.6	43	1	AA530920
C 35	20.2	54.6	45	9	AG194008
C 36	20.2	54.6	46	1	AA770617
C 37	20.2	54.6	50	1	AU105257
C 38	20.2	54.6	50	7	BN446714
C 39	20.2	54.6	52	8	BH630396
C 40	20.2	54.6	54	6	CB058194
C 41	20.4	54.1	34	8	AZ340626
C 42	20.4	54.1	38	9	CC799350
C 43	20.4	54.1	40	1	AI810174
C 44	20.4	54.1	41	8	AZ436472
C 45	20.4	54.1	45	8	AZ656574

ALIGNMENTS

RESULT 1
AA232965/c
LOCUS
DEFINITION
zr69a04.s1 Soares_NhMMPu_S1 Homo sapiens cdna clone IMAGE:668622 3', similar to SW:UCRX_BOVIN_P00130 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KD PROTEIN ;, mRNA sequence.
ACCESSION
AA232965
VERSION
AA232965.1 GI:1856126
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 55)
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE
WashU-Merck EST Project 1997
JOURNAL
Unpublished (1997)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert Length: 560 Std Error: 0.00
Seq primer: -a1m13 fwd. EF from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .55
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5563589"
/db_xref="taxon:9606"
/clone="IMAGE:668622"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhMMPu_S1"
/note="Organ: mixed (see below) ; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1123021 row: 16
Class: transposon-tagged.
Location/Qualifiers
1..43
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

144; Similarity 60.5%; Score 22.4; DB 9; Length 43;
114; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

1 GGGGACACCCUCCGCGGUNNNNNNGGCAU 32
|||||:|||||:|||||:|||||:|||||:
1 GGGTCTCTCTCTCGACCTCCATCGCGTGAT 42

H23825 49 bp mRNA linear EST 06-JUL-1995
IMAGE03.g1 Soares adult brain N2bSHB55Y Homo sapiens cDNA clone
YFAGE:173884 3, similar to SP:S39059 S39059 BRG1 PROTEIN -
;contains TAR1 repetitive element ;, mRNA sequence.
H23825
H23825.1 GI:892520
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1506
High quality sequence starts: 1

W269A01, mRNA sequence.	
CL214958	
CL214958.1 GI:40731859	
GSS.	
Mus musculus (house mouse)	
Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 53)	
Hansen,J., Flores,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.	
A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome	
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)	
22810117	
12904583	
Contact: GGTC	
German Genetrap Consortium (GGTC)	
Email: info@genetrap.de	
RosabetaGeo gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:	
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=W269A01' ES cell line harboring insertion mutation of target gene is available at:	
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'	
1' Inhouse Sequence Identifier: 12126	
Class: Gene Trap.	
Location/Qualifiers	
1..53	
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="129 Sv"	
/db_xref="taxon:10090"	
/clone="W269A01"	
/sex="Male"	
/cell_type="Embryonic stem cell"	
/cell_line="ES cells 129S2 (formerly 129/SvPas)"	
/clone_lib="GGTC Gene Trap Library GV04C04"	
/notes="Vector: ROSAbetaGeo"	
ORIGIN	
Query Match 58.4%; Score 21.6; DB 9; Length 53;	
Best Local Similarity 47.1%; Pred. No. 2.5e+05;	
Matches 16; Conservative 11; Mismatches 7; Indels 0; Gaps 0;	
QY 3 GUCCACUUCUGCGGUNNNNNNGGCGAUGC36	
51 GGCTCGGCTCGAGTGTCGCGGCGCGCGGT 18	
RESULT 12	
AI612870/c	
LOCUS	
DEFINITION	
tx20f12.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2269775 3' similar to TR:Q40503 Q40503 EXTENSIN. [1] ;contains MSRI.t1 MSRI repetitive element i; mRNA sequence.	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
EST.	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
1 (bases 1 to 58)	
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
AUTHORS	
TITLE	
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
Unpublished (1997)	
JOURNAL	
COMMENT	
Contact: Robert Strausberg, Ph.D.	
Email: cgapbs-r@mail.nih.gov	
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.	
cDNA Library Preparation: Life Technologies, Inc.	

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 869 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES

source
1. .58
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2269775"
/issue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH108"
/clone_lib="NCI CGAP Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

ORIGIN

Query Match 58.4%; Score 21.6; DB 1; Length 58;
Best Local Similarity 42.9%; Pred. No. 2.5e+05;
Matches 12; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

QY 10 UCCUCGCGUNNNNGGCGAUCGSBY 37
Db 49 TCGTCCGCGAGCAGGAGTGCAATCGCCT 22

RESULT 13

AA993587/c
LOCUS 49 bp mRNA linear EST 27-AUG-1998
DEFINITION Ot49g10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1619682
3' similar to TR:Q13748 Q13748 ALPHA-TUBULIN. [1] ;, mRNA sequence.

AA993587

AA993587.1 GI:3180132

VERSION Homo sapiens (human)

KEYWORDS Homo sapiens

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 49)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

UNPUBLISHED (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1291 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source
1. .49
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1619682"

/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTACCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTT 3'.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 57.3%; Score 21.2; DB 1; Length 49;
Best Local Similarity 44.1%; Pred. No. 3.5e+05;
Matches 15; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 4 UCCACUCCUGCGGUNNNNGGCGAUCGSBY 37

Db 39 TCCAGCCCCCAGCGTTGTCCCGGGGAACCTT 6

RESULT 14

TA234D12P
LOCUS 55 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 234d12, forward sequence,
genomic survey sequence.

ACCESSION AL481441

VERSION AL481441.1 GI:11847135

KEYWORDS GSS

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Trypanosoma

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 55)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. .55

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="234d12"

ORIGIN

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Best Local Similarity 53.8%; Pred. No. 3.5e+05;
Matches 14; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCACUCCUCCUGCGGUNNNNGGCG 30
||||:| ||||:|||||

Db 13 CCACATCTGCGGGTTAGCGACGGC 38

RESULT 15
CL234247
LOCUS 57 bp DNA linear GSS 08-JAN-2004
DEFINITION 02S0288-04D1-A12 UniformMu MuTAIL Library Zea mays genomic clone
ACCESSION CL234247
VERSION CL234247
KEYWORDS CL234247.1 GI:40778227
SOURCE GSS.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 57)
Lathaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
population
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
02S0288-04, Primer set: D
Class: transposon insertion site.
FEATURES
source
1..57
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xrefs="taxon:4577"
/clone="02S0288-04D1-A12"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match 57.3%; Score 21.2; DB 9; Length 57;
Best Local Similarity 46.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 5 CCACUCCUCCGGGUNNNNNNGGCGAUCGCB 36
Db 11 CCACGAGCTTGGCGAGTGACTGCGATGCGC 42

Search completed: March 15, 2005, 20:38:17
Job time : 1490.44 secs

1950-1951

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2	35.4	95.7	57	6	AX012282	Sequence	
3	35.4	95.7	57	6	AX012283	Sequence	
4	35.4	95.7	57	6	AX012284	Sequence	
5	35.4	95.7	57	6	AX012285	Sequence	
6	35.4	95.7	57	6	AX012286	Sequence	
7	35.4	95.7	57	6	AX012287	Sequence	
8	35.4	95.7	57	6	AX012288	Sequence	
9	35.4	95.7	57	6	AX012289	Sequence	
10	35.4	95.7	57	6	AX012290	Sequence	
c 11	30.2	81.6	866	14	HPDJS1	Hepatitis	
c 12	30.2	81.6	866	14	HPDJS2	Hepatitis	
c 13	30.2	81.6	911	14	HEB309874	Hepatitis	
c 14	30.2	81.6	934	14	HEB309875	Hepatitis	
c 15	30.2	81.6	1672	14	AB037947	Hepatitis	
c 16	30.2	81.6	1673	14	AB037948	Hepatitis	
c 17	30.2	81.6	1674	14	AB037949	Hepatitis	
c 18	30.2	81.6	1677	14	HPDAGE	Hepatitis	
c 19	30.2	81.6	1683	14	HDVJS3	Hepatitis	

RESULT 2	AX012282	AX012282	Sequence	44 from Patent WO9955856.	57 bp	RNA	linear	PAT 06-SEP-2000
LOCUS	AX012282	DEFINITION	AX012282	ACCESSION				
VERSION	AX012282.1	GI:9998343	KEYWORDS					
SOURCE		synthetic construct						
ORGANISM		synthetic construct						

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
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/note="synthetic nucleic acid"
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Best Local Similarity 59.5%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCGCGGUNNNNNNGGCGAUGCBSY 37
|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GGGTCCACCTCTCGCGGTCCGACCTGGGCATCGGCTT 37
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RESULT 3
AX012283
LOCUS AX012283 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 45 from Patent WO9955856.
ACCESSION AX012283
VERSION AX012283.1 GI:9998344
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
1..57
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/mol_type="unassigned RNA"
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Best Local Similarity 59.5%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCGCGGUNNNNNNGGCGAUGCBSY 37
|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GGGTCCACCTCTCGCGGTCCGACCTGGGCATCGGCG 37
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RESULT 4
AX012284
LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 95.7%; Score 35.4; DB 6; Length 57;
Best Local Similarity 59.5%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCGCGGUNNNNNNGGCGAUGCBSY 37
|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GGGTCCACCTCTCGCGGTCCGACCTGGGCATCGGCG 37
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RESULT 5
AX012285
LOCUS AX012285 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 47 from Patent WO9955856.
ACCESSION AX012285
VERSION AX012285.1 GI:9998346
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
1..57
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"
ORIGIN
Query Match 95.7%; Score 35.4; DB 6; Length 57;
Best Local Similarity 59.5%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGUCCACCUCUCGCGGUNNNNNNGGCGAUGCBSY 37
|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GGGTCCACCTCTCGCGGTCCGACCTGGGCATCGGCTT 37
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RESULT 6
AX012286
LOCUS AX012286 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 48 from Patent WO9955856.
ACCESSION AX012286
VERSION AX012286.1 GI:9998347
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
1..57
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"
ORIGIN
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HPDJS1	866 bp	linear	VRL 18-DEC-2002
LOCUS			
DEFINITION	Hepatitis D virus isolate:7/18/83	genomic RNA.	

1900-1901

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 15, 2005, 01:00:51 ; Search time 204.798 Seconds
(without alignments)
1069.494 Million cell updates/sec

Title: US-09-699-667E-65
Perfect score: 37
Sequence: 1 99gucacuccucggunnnnnnggcaugcsby 37

Scoring table: IDENTITY_NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11:	Geneseqn2003ds:*
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13:	Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35.4	95.7	37	AAZ57639	Aaz57639 Nucleotid
2	35.4	95.7	57	AAZ57636	Aaz57636 Trans-act
3	35.4	95.7	57	AAZ57638	Aaz57638 Trans-act
4	35.4	95.7	57	AAZ57637	Aaz57637 Trans-act
5	30.2	81.6	1688	ABZ77701	Abz77701 Nucleotid
6	30	81.1	48	ADR47040	Adr47040 Dengue vi
7	30	81.1	48	ADT48965	Adt48965 PCR prime
8	30	81.1	51	AAQ86173	Aaq86173 Primer HD
9	30	81.1	52	AAQ86204	Aaq86204 Sindbis/H
10	30	81.1	52	AAT31151	Aat31151 HDV rever
11	30	81.1	52	AAT30817	Aat30817 HDV riboz
12	30	81.1	52	AAV42394	Aav42394 Nested PC
13	30	81.1	52	AAV42426	Aav42426 Forward P
14	30	81.1	52	AAV60154	Aav60154 Nested PC
15	30	81.1	52	AAV60185	Aav60185 Reverse P
16	30	81.1	52	AAV70746	Aav70746 Reverse P
17	30	81.1	52	AAV70714	Aav70714 Nested pr
18	30	81.1	52	AAZ92930	Aaz92930 Hepatitis
19	30	81.1	52	AAZ92970	Aaz92970 Hepatitis
20	30	81.1	52	AAZ92843	Aaz92843 Hepatitis

21	30	81.1	52	3	AAZ92803	Hepatitis
22	30	81.1	52	6	AAZ38850	Alphaviru
23	30	81.1	52	6	AAZ38810	Alphaviru
24	30	81.1	52	6	ABK46276	HDV anti
25	30	81.1	52	6	ABK46316	Hepatitis
26	30	81.1	52	12	ADI30383	Hepatitis
27	30	81.1	52	12	ADI30423	Hepatitis
28	30	81.1	52	12	ADO13982	Eukaryoti
29	30	81.1	52	12	ADO13942	Eukaryoti
30	30	81.1	57	12	ADH10551	Hepatitis
31	30	81.1	80	2	AAQ53138	Substrate
32	30	81.1	80	2	AAQ53140	Substrate
33	30	81.1	83	5	AAF28121	HDV riboz
34	30	81.1	84	13	ADR47033	Dengue vi
35	30	81.1	85	2	AAQ46665	Self-clea
36	30	81.1	86	2	AAQ46663	Self-clea
37	30	81.1	90	2	AAQ76586	Hepatitis
38	30	81.1	90	5	AAF84035	EPO gene
39	30	81.1	90	5	AAF84036	EPO gene
40	30	81.1	91	8	ABZ82120	Hepatitis
41	30	81.1	94	12	ADP96249	HEP rabie
42	30	81.1	99	8	ABZ82121	Hepatitis
43	30	81.1	567	1	AAH82174	Clone del
44	30	81.1	1369	12	ADH10576	Nucleotid
45	30	81.1	1879	1	AAH82172	cDNA corr

ALIGNMENTS

RESULT 1	AAZ57639	standard; RNA; 37 BP.
ID	AAZ57639	standard; RNA; 37 BP.
XX	AAZ57639;	
AC	AAZ57639;	
XX	05-APR-2000	(first entry)
DT	05-APR-2000	(first entry)
XX	Nucleotide sequence of bimolecular ribozyme RZA fragment.	
DE	Nucleotide sequence of bimolecular ribozyme RZA fragment.	
XX	Bimolecular ribozyme; viral RNA cleavage; RZA fragment;	
KW	Bimolecular ribozyme; viral RNA cleavage; RZA fragment;	
KW	inherited disease; ss.	
XX	Synthetic.	
OS	Synthetic.	
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FT	misc_binding	1..6
FT		/tag= a
FT		/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT		/note= "Forms double-stranded region with bases 20-16 of sequence AAZ57640"
FT	stem_loop	7..19
FT		/tag= b
FT	misc_binding	20..25
FT		/tag= c
FT		/bound_moiety= "Ribozyme substrate Pl.1"
FT		/note= "Forms double-stranded region with bases 11-6 of sequence AAZ57641"
FT	misc_binding	30..37
FT		/tag= d
FT		/bound_moiety= "RzB fragment of bimolecular ribozyme"
FT		/note= "Forms double-stranded region with bases 8-1 of sequence AAZ57640"
PN	WO9955856-A2.	
XX	04-NOV-1999.	
PD	29-APR-1999;	99WO-CA000391.
XX	29-APR-1999;	98CA-02230203.
XX	(UYSH) UNIV SHERBROOKE.	

```

XX PI Perreault J, Ananvoranich S, Lafontaine D;
XX XX WPI; 2000-096791/08.
XX DR New construction of nucleic acid enzyme useful for biotechnological,
XX PT diagnostic and therapeutic applications.
XX PT Example 5; Fig 4; 52pp; English.
XX PS This is the nucleotide sequence bimolecular ribozyme Rza fragment. This
XX CC ribozyme cleaves substrate Sp1.1 (see AA257641). The invention relates to
XX CC a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
XX CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
XX CC substrate of the enzyme has the sequence 5'-H'-GNNHNN-3'. The binding
XX CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
XX CC cleavage site of the substrate (cleavage site is represented by *). At
XX CC least one nucleotide is present 5' to the cleavage site of the substrate
XX CC sequence. The enzyme of the invention is used to cleave a substrate
XX CC nucleotide sequence at a specific cleavage site by mixing the substrate
XX CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
XX CC for example an inherited disease. The enzymes also have other
XX CC therapeutic, biotechnological and diagnostic applications
XX SQ Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;

Query Match 95.7%; Score 35.4; DB 3; Length 37;
Best Local Similarity 73.0%; Pred. No. 0.39;
Matches 27; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGUNNNNNNGGCGAUGCGBY 37
DB 1 GGGUCCACCUCCUGCGGUGCCAGCCUGGCGGCC 37

RESULT 2
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
XX AC AAZ57636;
XX DT 05-APR-2000 (first entry)
XX DE Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
XX KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX KW inherited disease; deltaRzP1.1; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_binding 1..6
XX FT /*tag= a
XX FT /note= "Forms double stranded region with bases 52-57"
XX FT stem_loop 7..19
XX FT /*tag= b
XX FT misc_binding 20..25
XX FT /*tag= c
XX FT /bound_moiety= "SP1.1 substrate (AAZ57641) bases 5-11"
XX FT stem_loop 30..45
XX FT /*tag= d
XX FT misc_binding 52..57
XX FT /*tag= e
XX FT /note= "Forms a double stranded region with bases 6-1"
XX PN WO9955856-A2.
XX PD 04-NOV-1999.
XX XX 29-APR-1999; 99WO-CA000391.
XX PF 29-APR-1998; 98CA-02230203.
XX XX

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PA (UYSH ) UNIV SHERBROOKE.
XX PI Perreault J, Ananvoranich S, Lafontaine D;
XX XX WPI; 2000-096791/08.
XX DR New construction of nucleic acid enzyme useful for biotechnological,
XX PT diagnostic and therapeutic applications.
XX PT Example 1; Fig 1A; 52pp; English.
XX PS This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
XX CC cleaves substrate Sp1.1 (see AAZ57641). The invention relates to a
XX CC nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
XX CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
XX CC substrate of the enzyme has the sequence 5'-H'-GNNHNN-3'. The binding
XX CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
XX CC cleavage site of the substrate (cleavage site is represented by *). At
XX CC least one nucleotide is present 5' to the cleavage site of the substrate
XX CC sequence. The enzyme of the invention is used to cleave a substrate
XX CC nucleotide sequence at a specific cleavage site by mixing the substrate
XX CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
XX CC for example an inherited disease. The enzymes also have other
XX CC therapeutic, biotechnological and diagnostic applications
XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;

Query Match 95.7%; Score 35.4; DB 3; Length 57;
Best Local Similarity 73.0%; Pred. No. 0.42;
Matches 27; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCCUGCGGUNNNNNNGGCGAUGCGBY 37
DB 1 GGGUCCACCUCCUGCGGUGCCAGCCUGGCGGCC 37

RESULT 3
AAZ57638
ID AAZ57638 standard; RNA; 57 BP.
XX AC AAZ57638;
XX DT 15-SEP-2003 (revised)
XX DT 05-APR-2000 (first entry)
XX DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
XX KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX KW inherited disease; ss.
XX OS Hepatitis D virus.
XX FH Key Location/Qualifiers
XX FT misc_binding 1..6
XX FT /*tag= a
XX FT /note= "Forms double stranded region with bases 52-57"
XX FT stem_loop 7..19
XX FT /*tag= b
XX FT misc_binding 20..25
XX FT /*tag= c
XX FT /bound_moiety= "SP1.1 substrate bases (AAZ57641) 5-11"
XX FT stem_loop 30..45
XX FT /*tag= d
XX FT misc_binding 52..57
XX FT /*tag= e
XX FT /note= "Forms a double stranded region with bases 6-1"
XX PN WO9955856-A2.
XX PD 04-NOV-1999.
XX XX 29-APR-1999; 99WO-CA000391.
XX PF
XX XX

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PF	29-APR-1999;	99WO-CA000391.
XX		
PR	29-APR-1998;	98CA-02230203.
XX		
PA	(UYSH) UNIV SHERBROOKE.	
XX		
PI	Perreault J, Ananvoranich S, Lafontaine D;	
XX		
DR	WPI; 2000-096791/08.	
XX		
PT	New construction of nucleic acid enzyme useful for biotechnological,	
PT	diagnostic and therapeutic applications.	
XX		
PS	Example 1; Page; 52pp; English.	
XX		
CC	This is the nucleotide sequence of ribozyme deltaRzP1.2. This ribozyme	
CC	cleaves substrate SP1.2 (see AAZ57634). The invention relates to a	
CC	nucleic acid enzyme (e.g. deltaRzP1.2) that is constructed to have a	
CC	substrate binding portion with the following sequence 5'-H*GNNHNN-3'. The binding	
CC	portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the	
CC	cleavage site of the substrate (cleavage site is represented by *). At	
CC	least one nucleotide is present 5' to the cleavage site of the substrate	
CC	sequence. The enzyme of the invention is used to cleave a substrate	
CC	nucleotide sequence at a specific cleavage site by mixing the substrate	
CC	with the enzyme. The enzyme is used to cleave viral RNA or RNA causing	
CC	for example an inherited disease. The enzymes also have other	
CC	therapeutic, biotechnological and diagnostic applications. Note: This	
CC	sequence is not shown in the specification, but has been derived from the	
CC	deltaRzP1.1 sequence (AAZ57636) shown in figure 1	
XX		
SQ	Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;	
	Query Match 95.7%; Score 35.4; DB 3; Length 57;	
	Best Local Similarity 73.0%; Pred. No. 0.42;	
	Matches 27; Conservative 10; Mismatches 0; Indels 0; Gaps 0	
Qy	1 GGGUCCACCUCCUGCGGUNNNNNNGCGCAUGCSBY 37	
Db	1 GGGUCCACCUCCUGCGGUCGCCAGCGGCAUGCGGC 37	
RESULT 5		
ABZ77701/c		
ID	ABZ77701 standard; DNA; 1688 BP.	
XX		
AC	ABZ77701;	
XX		
DT	17-JUN-2003 (first entry)	
XX		
DE	Nucleotide sequence of the complete genome of HDV variant Pt62.	
XX		
KW	HDV; HDV dFr45; HDV dPr47; HDV dFr73; HDV dFr910; HDV dFr48; HDV dFr644;	
KW	satellite virus; HBV; SHD; LHD; antigenomic RNA; viral replication;	
XX	viral particle assembly; ss.	
XX		
OS	Hepatitis D virus.	
XX		
FN	FR2830019-A1.	
XX		
PD	28-MAR-2003.	
XX		
PF	24-SEP-2001; 2001FR-00012285.	
XX		
XX	24-SEP-2001; 2001FR-00012285.	
PR		
XX	(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.	
XX		
PA	Deny P, Radjef N, Huc AP;	
PI		
XX		
DR	WPI; 2003-365382/35.	
XX		
PT	New isolated nucleic acid from hepatitis D virus, useful for detection,	

PT diagnosis and phenotyping, also derived translation products and new
PT viral variants.
PS Disclosure; Page 89; 91pp; French.
XX
CC The present sequence represents the complete genome of a hepatitis D
CC virus (HDV) variant. The specification describes the genomes of HDV
CC variants dFr45, dFr47, dFr73, dFr910, dFr48, and dFr644. HDV is a
CC satellite virus of HBV, HDV replicates independently of HBV, and the only
CC two HDV proteins retrieved (sHD and LHD) code for antigenomic RNA. sHD
CC and LHD represent the short (24 kDa) and long (27 kDa) forms,
CC respectively, of the HDV protein. During replication, the functions of
CC these forms of the protein oppose each other: sHD plays an active role in
CC viral replication, while LHD stops it and plays a role in viral particle
CC assembly. Polynucleotides and polypeptides of HDV are useful for
CC detection and genotyping of hepatitis D virus, e.g. for diagnosis and
CC epidemiological monitoring
XX
SQ Sequence 1688 BP; 350 A; 505 C; 477 G; 356 T; 0 U; 0 Other;
Query Match 81.6%; Score 30.2; DB 8; Length 1688;
Best Local Similarity 54.5%; Pred. No. 50;
Matches 18; Conservative 14; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACUCCUCCGCGGNNNNNNNGGCAUGCSB 36
:|||||:|||||:|||||:|||||:|||||:|:
DB 893 TCCACCTCTCGCGTCCGACCTGGGCATCCGT 861
RESULT 6
ADR47040
ID ADR47040 standard; DNA; 48 BP.
XX
AC ADR47040;
XX
DT 18-NOV-2004 (first entry)
XX
DE Dengue virus vaccine oligonucleotide #15.
XX
KW ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
KW preM protein; C protein; NS1 protein signal; vaccine; cervical cancer;
KW viral disease; antigen; dendritic cell; immune response;
KW human papillomavirus.
XX
OS Unidentified.
XX
PN WO2004072274-A1.
XX
PD 26-AUG-2004.
XX
PF 30-JAN-2004; 2004WO-CN000088.
XX
PR 30-JAN-2003; 2003CN-00115272.
XX
PR 30-JAN-2003; 2003CN-00115273.
XX
PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA (TENG-) TENGGEN BIOMEDICAL CO.
PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX
PI Pang X;
XX
PI Pang X;
XX
DR WPI; 2004-625870/60.
XX
PT Virus-like particle vaccines containing dengue virus recombinant replicon
PT as core for carrier, applicable in preventives or/and remedies for tumors
PT like cervical cancer and viral diseases.
PS
XX Example 4; SEQ ID NO 37; 38pp; Chinese.
XX
CC A dengue virus recombinant replicon has a deletion of the complete coding
CC sequence for preM protein of dengue virus and also includes elements of
CC e.g. the non-coding region in the whole of the 5'-end, the coding region
CC of the front 20 amino acids in the C protein, and the coding region of

CC NS1 protein signal; coding regions of all non-structural proteins. The
CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pRS/FUJ2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to an oligonucleotide used in the
CC recombinant replicon of the invention.
XX
SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
Query Match 81.1%; Score 30; DB 13; Length 48;
Best Local Similarity 56.2%; Pred. No. 32;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACUCCUCCGCGGNNNNNNNGGCAUGCS 35
:|||||:|||||:|||||:|||||:|||||:|:
DB 17 TCCACCTCTCGCGTCCGACCTGGGCATCCG 48
RESULT 7
ADR48965
ID ADR48965 standard; DNA; 48 BP.
XX
AC ADR48965;
XX
DT 16-DEC-2004 (first entry)
XX
DE PCR primer 5' HDVr, seq id 29.
XX
KW Virucide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;
KW PCR; primer; ss.
XX
OS Viruses.
XX
PN WO2004082712-A1.
XX
PD 30-SEP-2004.
XX
PF 19-MAR-2004; 2004WO-CN000232.
XX
PR 20-MAR-2003; 2003CN-00115912.
XX
PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA (TENG-) TENGGEN BIOMEDICAL CO.
PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX
PI Pang X;
XX
PI Pang X;
XX
DR WPI; 2004-699719/68.
XX
XX Bivalent vaccines for preventing and treating Japanese (B) encephalitis
PT and hepatitis B produced by recombinant technique using encephalitis B
PT virus as vector to express antigen gene of hepatitis B.
XX
PS Example 8; SEQ ID NO 29; 33pp; Chinese.
XX
CC The invention relates to a recombinant Japanese encephalitis B virus
CC constructed from encephalitis B virus and a recombinant genome, where the
CC genome is inserted with an exogenous nucleotide sequence for
CC recombination and capable of retaining its self-replication function. The
CC virus is useful in producing the bivalent vaccines for preventing and
CC treating Japanese (B) encephalitis and hepatitis B. Such vaccines are
CC producible at low cost and have high immunoefficiency, in which the
CC recombinant virus can efficiently express the antigen of hepatitis B
CC virus with the safety and immunogenicity of attenuated encephalitis B
CC virus vaccines. The current sequence represents a PCR primer used in an

Qy
4 UCCACCUCCUGCGGUNNNNNNNGGCAUGCS 35


```

PT recombinant alpha:virus particles.
PS Example 3; Col 69; 140pp; English.
XX
CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC invention. The specification describes a DNA alphavirus structural
CC protein expression cassette which comprises an inducible promoter and an
CC alphavirus structural protein gene, where the promoter directs the
CC expression of the alphavirus structural protein gene upon induction of
CC the promoter within a cell, and where prior to induction within the cell,
CC the expression cassette does not express sufficient quantities of
CC structural proteins to be cytotoxic to a BHK cell containing the
CC expression cassette. The products may be used to inhibit pathogens and
CC stimulate an immune response
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
XX
Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGCGGTCGACCTGGGCATCCG 35
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
RESULT 13
AAV42426
ID AAV42426 standard; DNA; 52 BP.
XX
AC AAV42426;
XX
DT 02-OCT-1998 (first entry)
DE Forward PCR primer HDV17-68.
XX
KW DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; PCR primer; ss.
XX
OS Synthetic.
XX
XX US5789245-A.
XX
PD 04-AUG-1998.
XX
PF 30-OCT-1996; 96US-00741881.
XX
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX WPI; 1998-446089/38.
XX
XX DNA alpha:virus structural protein expression cassettes - for producing
XX recombinant alpha:virus particles.
XX
XX Example 7; Col 103; 140pp; English.
XX
CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
CC invention. The specification describes a DNA alphavirus structural
CC protein expression cassette which comprises an inducible promoter and an
CC alphavirus structural protein gene, where the promoter directs the
CC expression of the alphavirus structural protein gene upon induction of
CC the promoter within a cell, and where prior to induction within the cell,
CC the expression cassette does not express sufficient quantities of
CC structural proteins to be cytotoxic to a BHK cell containing the
CC expression cassette. The products may be used to inhibit pathogens and
CC stimulate an immune response
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
XX
Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGCGGTCGACCTGGGCATCCG 35
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32
RESULT 14
AAV60154
ID AAV60154 standard; DNA; 52 BP.
XX
AC AAV60154;
XX
DT 25-MAR-2003 (revised)
DT 04-DEC-1998 (first entry)
XX
DE Nested PCR primer HDV17-68.
XX
KW Eukaryotic layered vector initiation system; stimulate; immune response;
KW Sindbis; PCR primer; ss.
XX
OS Synthetic.
OS Hepatitis D virus.
XX
XX US5814482-A.
XX
PD 29-SEP-1998.
XX
PF 30-OCT-1996; 96US-00739158.
XX
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 14-SEP-1994; 94WO-US010469.
PR 30-NOV-1994; 94US-00348472.
PR 18-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
XX (POLO/) POLO J M.
XX (DUBE/) DUBENSKY T W.
XX (JOLLY) JOLLY D J.
XX (DRIV/) DRIVER D A.
XX
XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX WPI; 1998-541753/46.
XX
XX Eukaryotic layered vector initiation system - containing eukaryotic
XX promoter and heterologous antigen coding sequence, useful for stimulating
XX immune response.
XX
XX Example 3; Col 71-72; 144pp; English.
XX
CC PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
CC ribozyme sequence. The product is used in the course of the invention.
CC The specification describes an eukaryotic layered vector initiation
CC system, based on Sindbis. The eukaryotic layered vector initiation system
CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC susceptible target cell 5' to 3' synthesis of RNA from the viral cDNA.
CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX

```

SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
QY 4 UCCACCUCUCGCGGCGGCTCCGACCTGGGCATCCG 35
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1 TCCACCTCTCTCGGCGTCCGACCTGGGCATCCG 32
Search completed: March 15, 2005, 11:20:20
Job time : 204.798 secs

RESULT 15
AAV60185
ID AAV60185 standard; DNA; 52 BP.
XX AAV60185;
XX
XX 25-MAR-2003 (revised)
DT 04-DEC-1998 (first entry)
XX
XX Reverse PCR primer HDV17-68.
DE
XX Eukaryotic layered vector initiation system; stimulate; immune response;
KW Sindbis; PCR primer; ss.
KW
OS Synthetic.
XX
XX US5814482-A.
PN
XX
XX 29-SEP-1998.
PD
XX
XX 30-OCT-1996; 96US-00739158.
PF
XX
XX 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 14-SEP-1994; 94WO-US010469.
PR 30-NOV-1994; 94US-00348472.
PR 18-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
XX (POLO/) POLO J M.
PA (DUBE/) DUBENSKY T W.
PA (JOLL/) JOLLY D J.
PA (DRIV/) DRIVER D A.
XX
XX Driver DA, Polo JM, Jolly DJ, Dubensky TW;
PI
XX WPI; 1998-541753/46.
DR
XX Eukaryotic layered vector initiation system - containing eukaryotic
PT promoter and heterologous antigen coding sequence, useful for stimulating
PT immune response.
XX
XX Example 5; Col 108; 144pp; English.
PS
XX PCR primers AAV60184-85 are used in the course of the invention. The
XX specification describes an eukaryotic layered vector initiation system,
CC based on Sindbis. The eukaryotic layered vector initiation system
CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
SQ

Query Match 81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 33;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:18:52 ; Search time 61.3421 Seconds
(without alignments)
986.961 Million cell updates/sec

Title: US-09-699-667E-65
Perfect score: 37
Sequence: 1 ggguccaccuccggunnnnnnnngggaugcaby 37

Scoring table: IDENTITY NUCDX
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 240568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	81.1	52	1	US-08-741-881-40
2	30	81.1	52	1	US-08-741-881-80
3	30	81.1	52	1	US-08-739-158-40
4	30	81.1	52	1	US-08-739-158-80
5	30	81.1	52	2	US-08-739-167-40
6	30	81.1	52	2	US-08-739-167-80
7	30	81.1	52	3	US-08-404-796-40
8	30	81.1	52	3	US-08-404-796-80
9	30	81.1	52	3	US-08-931-869-40
10	30	81.1	52	3	US-08-931-869-80
11	30	81.1	52	3	US-09-350-399-40
12	30	81.1	52	3	US-09-350-399-80
13	30	81.1	52	3	US-09-236-140A-40
14	30	81.1	52	3	US-09-236-140A-80
15	30	81.1	80	1	US-08-238-963A-16
16	30	81.1	83	3	US-08-646-695-12
17	30	81.1	83	5	PCT-US96-06053-12
18	30	81.1	84	1	US-08-238-963A-13
19	30	81.1	84	1	US-08-238-963A-14
20	30	81.1	86	1	US-08-238-963A-6
21	30	81.1	90	4	US-09-554-337-2
22	30	81.1	90	4	US-09-733-042-12
23	30	81.1	90	4	US-09-733-042-13
24	30	81.1	101	6	5225337-2
25	30	81.1	101	6	5225337-2
26	30	81.1	105	2	US-08-553-619B-25
27	30	81.1	105	2	US-08-553-619B-30

28	30	81.1	8100	4	US-09-554-337-4	Sequence 4, Appli
29	30	81.1	14311	3	US-08-646-695-1	Sequence 1, Appli
c	30	81.1	14311	3	US-08-646-695-7	Sequence 7, Appli
31	30	81.1	14311	5	PCT-US96-06053-1	Sequence 1, Appli
c	30	81.1	14311	5	PCT-US96-06053-7	Sequence 7, Appli
32	30	81.1	14311	5	PCT-US96-06053-1	Sequence 1, Appli
33	30	81.1	15538	4	US-09-554-337-1	Sequence 1, Appli
34	29.2	78.9	85	1	US-08-238-963A-12	Sequence 12, Appli
35	29	78.4	56	3	US-09-415-784-39	Sequence 39, Appli
36	29	78.4	56	3	US-09-415-785A-39	Sequence 39, Appli
37	29	78.4	56	3	US-08-944-465-39	Sequence 39, Appli
38	29	78.4	56	3	US-09-415-868-39	Sequence 39, Appli
39	29	78.4	56	3	US-09-415-900-39	Sequence 39, Appli
40	29	78.4	56	4	US-09-507-362-39	Sequence 39, Appli
41	29	78.4	61	1	US-08-238-963A-18	Sequence 18, Appli
42	27	73.0	45	2	US-08-632-882-5	Sequence 5, Appli
43	27	73.0	45	4	US-09-419-125-5	Sequence 5, Appli
44	27	73.0	49	1	US-08-758-306-6	Sequence 6, Appli
45	27	73.0	49	3	US-08-985-162-1875	Sequence 1875, Ap

ALIGNMENTS

RESULT 1
US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

Query Match 81.1%; Score 30; DB 1; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCCGGUNNNNNNNNGGCAUGCS 35


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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-80

Query Match      81.1%; Score 30; DB 1; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNGGCAUGCS 35
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Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 5
US-08-739-167-40
; Sequence 40, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-40

Query Match      81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNGGCAUGCS 35
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Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 6
US-08-739-167-80
; Sequence 80, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-80
```

```
;
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-80

Query Match      81.1%; Score 30; DB 2; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNGGCAUGCS 35
   :||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 7
US-08-404-796-40
; Sequence 40, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-80
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/404,796
/ FILING DATE: 15-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-404-796-40

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCAUGCS 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 8

US-08-404-796-80
/ Sequence 80, Application US/08/404796
/ Patent No. 6015686
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/404,796
/ FILING DATE: 15-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear

US-08-404-796-80
Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCAUGCS 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 9

US-08-931-869-40
/ Sequence 40, Application US/08931869
/ Patent No. 6015694
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/931,869
/ FILING DATE: 16-SEP-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION NUMBER:
/ FILING DATE: 15-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-931-869-40

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNNNNNGGCAUGCS 35
:|||||:|||||:|||||:|||||:|||||:|
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 10

US-08-931-869-80
/ Sequence 80, Application US/08931869
/ Patent No. 6015694
/ GENERAL INFORMATION:

APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-80

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred.No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCGAUGCS 35
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Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 11
US-09-350-399-40
Sequence 40, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-350-399-40

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred.No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGCGGNNNNNGGCGAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 12
US-09-350-399-80
Sequence 80, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-350-399-80

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0;

QY 4 UCCACUCCUCGCGGNNNNNGGCGAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 13

US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.

TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-236-140A-40
Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0;

QY 4 UCCACUCCUCGCGGNNNNNGGCGAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 14

US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.

Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823.6000
TELEFAX: (949) 823.6100

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match 81.1%; Score 30; DB 3; Length 52;
Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 18; Conservative 13; Mismatches 1; Indels 0;

QY 4 UCCACUCCUCGCGGNNNNNGGCGAUGCS 35
:||||:||||:||||:||||:||||:|
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 15

US-08-238-963A-16
; Sequence 16, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMATIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,963A

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; FILING DATE: May 5, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/821,155
; FILING DATE: January 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-238-963A-16

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Query Match      81.1%; Score 30; DB 1; Length 80;
Best Local Similarity 71.9%; Pred. No. 9;
Matches 23; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
QY      4 UCCACCUCCUGCGGUNNNNNNGGCGAUGCS 35
Db      8 UCCACCUCCUGCGGUGCGACUGGCGAUCG 39

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Search completed: March 15, 2005, 15:26:40
Job time : 62.3421 secs

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:06:47 ; Search time 1607.39 Seconds
(without alignments)
876.189 Million cell updates/sec

Title: US-09-699-667E-65
Perfect score: 37
Sequence: 1 ggguccaccucccggunnnnnnnnggcaugcaby 37

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
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7: gb_est6: *
8: gb_gse1: *
9: gb_gse2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	28	75.7	490	1	AI192713 GE67C07.x
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C 4	28	75.7	595	2	AW970713 EST382796
C 5	28	75.7	899	2	BF673679 602136403
C 6	28	75.7	1029	5	BQ889958 AGENCOURT
C 7	28	75.7	1029	5	AY401937 Homo sapi
C 8	27.8	75.1	559	2	BE724383 894075F05
C 9	27.4	74.1	338	4	BM660932 952043A11
C 10	27.4	74.1	476	4	BM134274 WHE0488.A
C 11	27.4	74.1	477	8	BZ894888 Hg4_0179
C 12	27.4	74.1	515	6	CA601344 w11.pk001
C 13	27.4	74.1	586	2	BE445167 WHE1132.B
C 14	27.4	74.1	603	9	CC698821 OGUU757H
C 15	27.4	74.1	628	4	BM660931 952043A11
C 16	27.4	74.1	697	8	BH880075 RL50H02.b
C 17	27.4	74.1	773	9	CC698827 OGUU757V
C 18	27.4	74.1	808	2	AZ125162 OSJNB007
C 19	27.4	74.1	810	8	BF687835 602066894
C 20	27.4	74.1	855	9	CG353689 OGYBN42TV
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C 23	27.4	74.1	976	9	CG175771 PUKC138TB
C 24	27.4	74.1	998	9	CG226930 OGWG80TV

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C 31	27	73.0	590	4	BI528255
C 32	27	73.0	604	4	BG556388
C 33	27	73.0	686	9	LBAP033B03
C 34	27	73.0	694	4	BG859346
C 35	27	73.0	726	9	CNS02J2N
C 36	27	73.0	729	9	CL154836
C 37	27	73.0	748	9	CG207019
C 38	27	73.0	750	9	CL154835
C 39	27	73.0	757	8	BZ638091
C 40	27	73.0	796	1	AI069049
C 41	27	73.0	812	8	BZ734785
C 42	27	73.0	828	9	CC692415
C 43	27	73.0	967	8	CC374631
C 44	26.8	72.4	313	1	AA421385
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ALIGNMENTS

RESULT 1
LOCUS BQ360043/c 396 bp mRNA linear EST 20-MAY-2002
DEFINITION PM1-HN0079-100101-005-d10 HN0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ360043
VERSION BQ360043.1 GI:21028363
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,D.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM1&t2=PM1-HN0079-100101-005-d10&t3=2001-01-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 55.
Location/Qualifiers
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HN0079"

/note="Organ: head normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products


```

REFERENCE
AUTHORS      Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
              Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
              Quackenbush,J.
TITLE        Assessment of gene expression patterns in a model of colon tumor
              metastasis using a 19,200 element cDNA microarray
JOURNAL      Unpublished (2000)
COMMENT      Contact: John Quackenbush
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 3528
              Fax: 301 838 0208
              Email: johnq@igr.org
              Plate: 281
              Seq primer: Forward.
              Location/Qualifiers
                1..595
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="MAGE resequencences, MAGK"
                /note="Vector: pBluescriptSKm"

ORIGIN
Query Match      75.7%; Score 28; DB 2; Length 595;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 14; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGUCCACUCCUCCGGGCGGNNNNNNNGGCGCAUCGSBY 37
    ||:||||:||||:||||:||||:||||:||||:||||:|
Db 452 GGTTCACCTCTCCGCGGTCGATCGCGTCGAGCAGC 417

RESULT 5
BF673679/c
LOCUS      BF673679
DEFINITION BF673679
ACCESSION BF673679
VERSION    BF673679.1 GI:11947574
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 899)
            NIH-MGC http://mgi.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1087 row: f column: 01
            High quality sequence stop: 585.
            Location/Qualifiers
              1..899
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:4272768"
              /lab_host="DH10B (T1 phage-resistant)"
              /clone_lib="NIH MGC 83"
              /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
              Site_1: SfiI (ggccgctcgcc); Site_2: SfiI
              (ggccatcgcc); 5' and 3' adaptors were used in cloning
              as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3'
              and 3' adaptor sequence:

REFERENCE
AUTHORS      Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
              Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
              Quackenbush,J.
TITLE        Assessment of gene expression patterns in a model of colon tumor
              metastasis using a 19,200 element cDNA microarray
JOURNAL      Unpublished (2000)
COMMENT      Contact: John Quackenbush
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 3528
              Fax: 301 838 0208
              Email: johnq@igr.org
              Plate: 281
              Seq primer: Forward.
              Location/Qualifiers
                1..595
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="MAGE resequencences, MAGK"
                /note="Vector: pBluescriptSKm"

ORIGIN
Query Match      75.7%; Score 28; DB 2; Length 595;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 14; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGUCCACUCCUCCGGGCGGNNNNNNNGGCGCAUCGSBY 37
    ||:||||:||||:||||:||||:||||:||||:||||:|
Db 452 GGTTCACCTCTCCGCGGTCGATCGCGTCGAGCAGC 417

RESULT 6
BQ889958/c
LOCUS      BQ889958
DEFINITION BQ889958
ACCESSION BQ889958
VERSION    BQ889958.1 GI:22281972
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 1029)
            NIH-MGC http://mgi.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM13567 row: m column: 14
            High quality sequence stop: 456.
            Location/Qualifiers
              1..1029
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:6182197"
              /sex="male"
              /tissue_type="dorsal root ganglia"
              /dev_stage="adult, 36 yr"
              /lab_host="DH10B"
              /clone_lib="Lupski dorsal root ganglion"
              /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
              NotI; Site_2: Sali; cDNA made by oligo-dT priming.
              Directionally cloned using the following adaptors:
              5'-TCGACCCACGCGTCCG-3' and
              5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
              1 kb for average insert length 1.7 kb. This is a primary
              library, non-amplified. Library constructed by Life
              Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
              College of Medicine) and is available through Life
              Technologies."

FEATURES
source
BF673679
602136403F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272768 5',
mRNA sequence.
BF673679.1 GI:11947574
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 899)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1087 row: f column: 01
High quality sequence stop: 585.
Location/Qualifiers
1..899
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4272768"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgctcgcc); Site_2: SfiI
(ggccatcgcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3'
and 3' adaptor sequence:

FEATURES
source
BQ889958
8228912 Lupski dorsal root ganglion Homo sapiens cDNA
clone IMAGE:6182197 5', mRNA sequence.
BQ889958
BQ889958.1 GI:22281972
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1029)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM13567 row: m column: 14
High quality sequence stop: 456.
Location/Qualifiers
1..1029
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6182197"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: Sali; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

FEATURES
source
GGUCCACUCCUCCGGGCGGNNNNNNNGGCGCAUCGSBY 37
||:||||:||||:||||:||||:||||:||||:||||:|
GGTTCACCTCTCCGCGGTCGATCGCGTCGAGCAGC 299

```

COURT


```

/lab_host="DH10B"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced
rRNA)"
/notes="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The
library was prepared by George Rudenko using poly (A)
selected RNA and Universal Riboclone cDNA Synthesis System
(Promega). cDNA was synthesized using both random and
oligo(dT) primers in separate reactions and equipped with
EcoRI adaptors. Library was size-fractionated on agarose
gels (for insert size >400bp) and non-directionally cloned
into EcoRI-digested pUC19 vector. Blue/white selection on
carbenicillin-containing plates was used to recover
positive clones."

```

```

ORIGIN
Positive clones.
Query Match          74.1%; Score 27.4; DB 4; Length 338;
Best Local Similarity 48.6%; Pred. No. 2.2e+03;
Matches 18; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

QY      1  GGGUCCACCUCCUGCGGUNNNNNNGGCGAUGCSBY 37
      |||||:||||:||||:||||:||||:||||:
DB      164  GGGTCACAGTCCTCGGCCCTCGCAGAGGACGACCGGT 128

```

RESULT 10	BM134274	476 bp	mRNA	linear	EST 28-NOV-2001
LOCUS	BM134274				
DEFINITION	WHE0488_A04_A082S wheat Fusarium graminearum infected spike cDNA library Triticum aestivum cDNA clone WHE0488_A04_A08, mRNA sequence.				

ACCESSION	SEQUENCE
BMI34274	BMI34274
VERSION	BMI34274.1 GI:17141848
KEYWORDS	EST.
SOURCE	Triticum aestivum (bread wheat)
ORGANISM	Triticum aestivum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
REFERENCE	1 (bases 1 to 476)
AUTHORS	Anderson,O.D., Chao,S., Han,P.S., Heinen,S., Hsia,C.C., Kang,Y., Kruger,W.M., Lazo,G.R., Miller,S., Muehlbauer,G.J., Miller,R., Pritsch,C., Rausch,C.J., Seaton,C.L., Tong,J.C., Vance,C. and Wilson,C.F.

TITLE	The structure and function of the expressed portion of the wheat genomes - <i>Fusarium graminearum</i> infected spike cDNA library
JOURNAL	Unpublished (2001)
COMMENT	Contact: Olin Anderson

Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@pw.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20. No effort was taken
 to identify ESTs of fungal origin from this library, thus this EST
 could be of wheat or fungal origin.
 Seq primer: StrataGene SK primer.

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FEATURES
    source
        Location/Qualifiers
            1. .476
                /organism="Triticum aestivum"
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                /cultivar="Sumai3"
                /db_xref="taxon:4565"
                /clone="WHE0488_A04_A08"
                /tissue_type="Spike"
                /dev_stage="Adult plant"
                /lab_host="E. coli SOLR"
                /clone_lib="Wheat Fusarium graminearum infected spike cDNA
                library"
            /notes="Vector: Lambda Uni-ZAP XR, excised phagemid
            pluescript SK; Site:1: EcoRI; Site:2: XhoI; Plants were
            grown in the greenhouse. Spikes were spraved at anthesis

```

with Fusarium graminearum. Total RNA, and poly(A) RNA were prepared and pooled from infected spike at 0, 6, 12, 24, 36 and 48 hours after inoculation, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in G. Muehlbauer lab at the University of Minnesota (Kruger, W.M., Muehlbauer, G.J., Pritsch, C., Vance, C.). The cDNA library should contain genes of both wheat and fungal pathogen origin. Plasmid DNA preparations and DNA sequencing were performed in the ON Anderson lab (all other authors).

```

ORIGIN
      74.1%; Score 27.4; DB 4; Length 476;
Query Match      48.6%; Pred. No. 2.2e+03;
Best Local Similarity
Matches 18; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

QY      1  GGGUCCACUCCUCGCGGUNNNNNNGGCGAUCGSBY 37
      | | | | | | | | | | | | | | | | | | | |
Db      112  GCGTCACCTCTCGTCGACGATGCCGCGCATGCTTT 148

```

RESULT 11				
BZ894888/c				
LOCUS	BZ894888	477 bp	DNA	linear
DEFINITION	Hg4_0179 Hg pUC18 Library Halobaculum gomorrense genomic 5', genomic survey sequence.			

Genomic survey sequence.	
ACCESSION	BZ894888
VERSION	BZ894888.1
KEYWORDS	GI:333345364
SOURCE	GSS.
ORGANISM	Halobaculum gomorrense
REFERENCE	Halobaculum gomorrense
AUTHORS	Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Halobaculum.
TITLE	1 (bases 1 to 477)
COMMENT	Goo Y., Roach, J., Glusman, G., Baliga, N.S., Deutsch, K., Pan, M., Dasgama, S., Ng, W.V. and Hood, L.
	Low-pass Sequencing for Microbial Comparative Genomics
	Unpublished (2003)
	Contact: Goo Y

Contact: Yvonne
Institute for Systems Biology
1441 North 34th Street, Seattle, WA 98103, USA
Tel: 206 732 1412
Fax: 206 732 1299
Email: Yvonne@systemsbiology.org
Seq primer: M13 Forward
Class: shotgun.

```

Class: smc-gun:
Location/Qualifiers
1. .477
/organism="Halobaculum gomorrense"
/mol_type="genomic DNA"
/strain="ATCC 700876"
/db_xref="taxon:43928"
/clone_lib="Hg pUC18 library"
/note="Vector: pUC18; Site: 1:
constructed from Halobaculum gomorrense genomic DNA using
pUC18/SmaI/BAP plasmid"

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Query Match      74.1%; Score 27.4; DB 8; Length 477;
Best Local Similarity 54.1%; Pred.No.2.2e+03;
Matches 20; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY      1 GGGUCCACUCUCGCGGUNNNNNNGGCAUGCBSY 37
Db      450 GGGTTCACCCCTCGCCCTCGGCGNCCGACGCGGT 414

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RESULT 12	CA601344	515 bp	mRNA	linear	EST 21-NOV-2002
LOCUS	CA601344				
DEFINITION	wll.pk0012.b7 wll Triticum aestivum cDNA clone wll.pk0012.b7 5' end, mRNA sequence.				
ACCESSION	CA601344				


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/db_xref="taxon:4577"
/clone="ZMMBMA0424M05"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBSCk; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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ORIGIN

Query Match 74.1%; Score 27.4; DB 9; Length 603;
Best Local Similarity 48.6%; Pred. No. 2.2e+03;
Matches 18; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGUCCACCUCCUGCGGUNNNNNNGGCAUGCSB 37
Db 398 GGGTTCACGTCTCGCCTCGAGAGGACGCGCGT 362

RESULT 15	BM660931	LOCUS	628 bp	mRNA	linear	EST 27-FEB-2002
DEFINITION	952043A11.x1 952	- BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.				

ACCESSION BM660931
VERSION BM660931.1
KEYWORDS GI:18964309
EST.

ORGANISM	Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	1 (bases 1 to 628)
REFERENCE	

REFERENCE
1 (bases 1 to 628)
Walbot, V.
AUTHORS
Maize ESTs from various cDNA libraries sequenced at Stanford
TITLE

```

FEATURES
  source
    Location/Qualifiers
      1. .628
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="BMS (Black Mexican Sweet)"
        /db_xref="taxon:4577"
        /tissue_type="suspension culture"
        /dev_stage="mixed logarithmic and stationary growth
          phases"
        /lab_host="DH10B"
        /clone_lib="952 - BMS tissue from Walbot Lab (reduced
          rRNA)"

```

IRNA) "Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

ORIGIN	74.1%;	Score 27.4;	DB 4;	Length 628;
Query Match	48.6%;	Pred. No. 2.2e+03;		
Best Local Similarity	14;	Mismatches 5;	Indels 0;	Gaps 0;
Matches 18;	Conservative			

Accession	Protein	Length	Score	E-value
QY	1 GGGCCACCCUCCGCGGUNNNNNNGGCAUGCSBY	37		
	574 GGTTCACAGTCTCTCGCCCTCGCAGGAGGACGCGGT	610		

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:26:58 ; Search time 33.2456 Seconds
(without alignments)
984.356 Million cell updates/sec

Title: US-09-699-667E-66

Perfect score: 20

Sequence: 1 bkscaugcguaaggacc 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1250976

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_5/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_5/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_5/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_5/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_5/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_5/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	72.0	39	1 US-08-096-027-4	Sequence 4, Appli
2	14.4	72.0	39	1 US-08-461-725-4	Sequence 4, Appli
3	14.4	72.0	39	1 US-08-460-981-4	Sequence 4, Appli
C 4	13.8	69.0	27	3 US-09-073-492-5	Sequence 5, Appli
C 5	13.8	69.0	48	1 US-08-741-881-41	Sequence 41, Appli
C 6	13.8	69.0	48	1 US-08-739-158-41	Sequence 41, Appli
C 7	13.8	69.0	48	2 US-08-739-167-41	Sequence 41, Appli
C 8	13.8	69.0	48	3 US-08-404-796-41	Sequence 41, Appli
C 9	13.8	69.0	48	3 US-08-931-869-41	Sequence 41, Appli
C 10	13.8	69.0	48	3 US-09-350-399-41	Sequence 41, Appli
C 11	13.8	69.0	48	3 US-09-236-140A-41	Sequence 41, Appli
C 12	13.8	69.0	56	1 US-08-741-881-79	Sequence 79, Appli
C 13	13.8	69.0	56	1 US-08-739-158-79	Sequence 79, Appli
C 14	13.8	69.0	56	2 US-08-739-167-79	Sequence 79, Appli
C 15	13.8	69.0	56	3 US-08-404-796-79	Sequence 79, Appli
C 16	13.8	69.0	56	3 US-08-931-869-79	Sequence 79, Appli
C 17	13.8	69.0	56	3 US-09-350-399-79	Sequence 79, Appli
C 18	13.8	69.0	56	3 US-09-236-140A-79	Sequence 79, Appli
C 19	13.6	68.0	35	1 US-07-832-905B-80	Sequence 80, Appli
C 20	13.6	68.0	35	2 US-08-700-757-80	Sequence 80, Appli
C 21	13.6	68.0	43	1 US-07-832-905B-81	Sequence 81, Appli
C 22	13.6	68.0	43	2 US-08-700-757-81	Sequence 81, Appli
C 23	13.6	68.0	47	1 US-08-171-389-282	Sequence 282, App
C 24	13.6	68.0	47	1 US-08-123-936-282	Sequence 282, App
C 25	13.6	68.0	47	2 US-08-475-228A-282	Sequence 282, App
C 26	13.6	68.0	47	3 US-08-482-080A-282	Sequence 282, App
C 27	13.6	68.0	47	3 US-09-354-947-282	Sequence 282, App

Sequence 282, App
Sequence 306, App
Sequence 306, App
Sequence 307, App
Sequence 307, App
Sequence 10, Appl
Sequence 10299, A
Sequence 10300, A
Sequence 33, Appl
Sequence 67, Appl
Sequence 27956, A
Sequence 18244, A
Sequence 48582, A
Sequence 48584, A
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-08-096-027-4
; Sequence 4, Application US/08096027
; Patent No. 5591632
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael A.
; APPLICANT: Duda, Rosemary B.
; APPLICANT: Dewolf, William C.
; APPLICANT: Aldovini, Anna
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: RECOMBINANT BCG VACCINES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,027
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,334
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/367,894
; FILING DATE: 19-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/03451
; FILING DATE: 18-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/02962
; FILING DATE: 07-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/361,944
; FILING DATE: 05-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/223,089
; FILING DATE: 22-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/216,390
; FILING DATE: 07-JUL-1988
; PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: US 07/163,546
;/ FILING DATE: 03-MAR-1988
;/ PRIOR APPLICATION DATA: PCT/US88/00614
;/ APPLICATION NUMBER: PCT/US88/00614
;/ FILING DATE: 29-FEB-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/020,451
;/ FILING DATE: 02-MAR-1987
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Granahan, Patricia
;/ REGISTRATION NUMBER: 32,227
;/ REFERENCE/DOCKET NUMBER: WH189-05A2
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617) 861-6240
;/ TELEFAX: (617) 861-9540
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 39 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
;/ US-08-096-027-4

Query Match 72.0%; Score 14.4; DB 1; Length 39;
Best Local Similarity 77.8%; Pred. No. 4.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SGCAUGGCUAAGGACCC 20
:|||||:|||||:
Db 1 GGCATGGCCAAGGATCC 18

RESULT 2

US-08-461-725-4
; Sequence 4, Application US/08461725
; Patent No. 5776465
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael A.
; APPLICANT: Duda, Rosemary B.
; APPLICANT: DeWolf, William C.
; APPLICANT: Aldovini, Anna
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: RECOMBINANT BCG VACCINES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,725
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,027
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,334
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA: US 07/367,894
; FILING DATE: 19-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/03451
; FILING DATE: 18-JUN-1990

;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US89/02962
;/ FILING DATE: 07-JUL-1989
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/361,944
;/ FILING DATE: 05-JUN-1989
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/223,089
;/ FILING DATE: 22-JUL-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/216,390
;/ FILING DATE: 07-JUL-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/163,546
;/ FILING DATE: 03-MAR-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US88/00614
;/ FILING DATE: 29-FEB-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/020,451
;/ FILING DATE: 02-MAR-1987
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Granahan, Patricia
;/ REGISTRATION NUMBER: 32,227
;/ REFERENCE/DOCKET NUMBER: WH189-05A2
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617) 861-6240
;/ TELEFAX: (617) 861-9540
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 39 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
;/ US-08-461-725-4

Query Match 72.0%; Score 14.4; DB 1; Length 39;
Best Local Similarity 77.8%; Pred. No. 4.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SGCAUGGCUAAGGACCC 20
:|||||:|||||:
Db 1 GGCATGGCCAAGGATCC 18

RESULT 3

US-08-460-981-4
; Sequence 4, Application US/08460981
; Patent No. 5830475
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael A.
; APPLICANT: Duda, Rosemary B.
; APPLICANT: DeWolf, William C.
; APPLICANT: Aldovini, Anna
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: RECOMBINANT BCG VACCINES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,981
; FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,027
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,334
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,894
FILING DATE: 19-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/03451
FILING DATE: 18-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02962
FILING DATE: 07-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/361,944
FILING DATE: 05-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/223,089
FILING DATE: 22-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/216,390
FILING DATE: 07-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/163,546
FILING DATE: 03-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US88/00614
FILING DATE: 29-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/020,451
FILING DATE: 02-MAR-1987
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH189-05A5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-460-981-4

Query Match 72.0%; Score 14.4; DB 2; Length 39;
Best Local Similarity 77.8%; Pred. No. 4.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SGCAUGGCUAAGGACCC 20
Db 1 GGCATGCCCAAGGGATCC 18

RESULT 4
US-09-073-492-5/c
Sequence 5, Application US/09073492
Patent No. 6248578
GENERAL INFORMATION:
APPLICANT: Banerjee, Amiya K.
APPLICANT: Hoffman, Michael A.
TITLE OF INVENTION: Infectious Clone for Human Parainfluenza
TITLE OF INVENTION: Virus Type 3
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold LLP
STREET: 800 Superior Avenue

CITY: Cleveland
STATE: Ohio
COUNTRY: USA
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,492
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 23114/04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216)622-8200
TELEFAX: (216)241-0816
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-073-492-5

Query Match 69.0%; Score 13.8; DB 3; Length 27;
Best Local Similarity 64.7%; Pred. No. 8.6e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17
Db 26 CTCGGATGGCTAAGGA 10

RESULT 5
US-08-741-881-41/c
Sequence 41, Application US/08741881
Patent No. 5789245
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,881
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-41

Query Match 69.0%; Score 13.8; DB 1; Length 48;
Best Local Similarity 64.7%; Pred. No. 9.1e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 BKSGCAUGGCUAAGGA 17
Db 29 CTCGGATGGCTAAGGA 13

RESULT 6

US-08-739-158-41/c
; Sequence 41, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-41

Query Match 69.0%; Score 13.8; DB 1; Length 48;
Best Local Similarity 64.7%; Pred. No. 9.1e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 BKSGCAUGGCUAAGGA 17
Db 29 CTCGGATGGCTAAGGA 13

RESULT 7

US-08-739-167-41/c
; Sequence 41, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-41

Query Match 69.0%; Score 13.8; DB 2; Length 48;
Best Local Similarity 64.7%; Pred. No. 9.1e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 BKSGCAUGGCUAAGGA 17
Db 29 CTCGGATGGCTAAGGA 13

RESULT 8

US-08-404-796-41/c
; Sequence 41, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US


```
/
/
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/404,796
/ FILING DATE: 15-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-404-796-41
/
/ Query Match 69.0%; Score 13.8; DB 3; Length 48;
/ Best Local Similarity 64.7%; Pred. No. 9.1e+02;
/ Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 1 BKSGCAUGGCUAAGGA 17
/ DB 29 CTCGGATGCGTAAGGA 13
/
/ RESULT 9
/ US-09-931-869-41/c
/ Sequence 41, Application US/08931869
/ Patent No. 6015694
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/931,869
/ FILING DATE: 16-SEP-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/404,796
/ FILING DATE: 15-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
```

```
/
/
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-931-869-41
/
/ Query Match 69.0%; Score 13.8; DB 3; Length 48;
/ Best Local Similarity 64.7%; Pred. No. 9.1e+02;
/ Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 1 BKSGCAUGGCUAAGGA 17
/ DB 29 CTCGGATGCGTAAGGA 13
/
/ RESULT 10
/ US-09-350-399-41/c
/ Sequence 41, Application US/09350399
/ Patent No. 6342372
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/350,399
/ FILING DATE: 08-Jul-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:
/ US-09-350-399-41
/
/ Query Match 69.0%; Score 13.8; DB 3; Length 48;
/ Best Local Similarity 64.7%; Pred. No. 9.1e+02;
/ Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 1 BKSGCAUGGCUAAGGA 17
/ DB 29 CTCGGATGCGTAAGGA 13
/
/ RESULT 11
/ US-09-236-140A-41/c
/ Sequence 41, Application US/09236140A
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US-08-739-158-79

Query Match 69.0%; Score 13.8; DB 1; Length 56;
Best Local Similarity 64.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGA 17
DB 37 CTCGGATGGCTAAGGA 21

RESULT 14

US-08-739-167-79/c
; Sequence 79, Application US/08739167
; Patent No. 5843723

; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W

; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.

; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.

; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.

; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.

; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-739-167-79

Query Match 69.0%; Score 13.8; DB 2; Length 56;
Best Local Similarity 64.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGA 17
DB 37 CTCGGATGGCTAAGGA 21

RESULT 15

US-08-404-796-79/c
; Sequence 79, Application US/08404796
; Patent No. 6015686

; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W

; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 06:19:02 ; Search time 392.807 Seconds
(without alignments)
2467.126 Million cell updates/sec

Title: US-09-699-667E-66
Perfect score: 20
Sequence: 1 bksgaugcuaaggagccc 20
Scoring table: IDENTITY_NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	57	6	AX012282 Sequence
2	18.4	92.0	57	6	AX012283 Sequence
3	18.4	92.0	57	6	AX012284 Sequence
4	18.4	92.0	57	6	AX012285 Sequence
5	18.4	92.0	57	6	AX012286 Sequence
6	18.4	92.0	57	6	AX012287 Sequence
7	18.4	92.0	57	6	AX012288 Sequence
8	18.4	92.0	57	6	AX012289 Sequence
9	18.4	92.0	57	6	AX012290 Sequence
10	17.6	88.0	18	6	AX012292 Sequence
11	17.2	86.0	236594	2	AC118386 Rattus no
12	16.8	84.0	159629	9	AC098616 Homo sapi
13	16.8	84.0	177226	10	AC121858 Mus muscu
14	16.8	84.0	195568	9	AC092503 Homo sapi
15	16.6	83.0	144393	2	AC108403 Mus muscu
16	16.6	83.0	156356	10	AC132314 Mus muscu
17	16.6	83.0	251908	2	AC094522 Rattus no
18	16	80.0	2100	1	XANAVR M32142 X.campestri
19	16	80.0	10992	1	AE012317 Xanthomon

20	16	80.0	234909	2	AC094325	AC094325 Rattus no
c 21	16	80.0	244389	2	AC111858	AC111858 Rattus no
c 22	16	80.0	253409	2	AC095230	AC095230 Rattus no
23	16	80.0	255367	2	AC121743	AC121743 Rattus no
24	16	80.0	256219	2	AC095416	AC095416 Rattus no
25	16	80.0	275551	2	AC132049	AC132049 Rattus no
c 26	15.8	79.0	1158	6	C0732886	C0732886 Sequence
27	15.8	79.0	1188	5	AF492508	AF492508 Aeronauts
28	15.8	79.0	1188	5	AF492513	AF492513 Tachornis
c 29	15.8	79.0	11725	6	AR070467	AR070467 Sequence
c 30	15.8	79.0	11725	6	I05479	I05479 Sequence 13
c 31	15.8	79.0	11725	6	I07993	I07993 Sequence 1
c 32	15.8	79.0	11725	6	AR390800	AR390800 Sequence
c 33	15.8	79.0	11725	6	AR474619	AR474619 Sequence
c 34	15.8	79.0	11725	9	HUMPRCA	M11228 Human prote
c 35	15.8	79.0	13870	6	AX959240	AX959240 Sequence
c 36	15.8	79.0	13870	9	AF378903	AF378903 Homo sapi
c 37	15.8	79.0	29188	9	HS77019	AL035609 Human DNA
c 38	15.8	79.0	104228	9	AL354751	AL354751 Human DNA
c 39	15.8	79.0	110000	2	AL114447	Continuation (3 of
c 40	15.8	79.0	123413	9	AL138834	AL138834 Human DNA
41	15.8	79.0	134127	2	AC087119	AC087119 Mus muscu
c 42	15.8	79.0	150622	9	AL390203	AL390203 Human DNA
c 43	15.8	79.0	163924	2	AL162592	AL162592 Homo sapi
c 44	15.8	79.0	164741	2	AC027278	AC027278 Mus muscu
45	15.8	79.0	172117	10	AC115040	AC115040 Mus muscu

ALIGNMENTS

RESULT 1
AX012282
LOCUS AX012282
DEFINITION Sequence 44 from Patent WO9955856.
ACCESSION AX012282
VERSION AX012282.1 GI:9998343
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANTICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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/note="synthetic nucleic acid"

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QY 1 BKSGCAUGGCTUAGGAGCCC 20
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Db 38 TTCGCATGGCTAAGGAGCCC 57

RESULT 2

AX012283
LOCUS AX012283
DEFINITION Sequence 45 from Patent WO9955856.
ACCESSION AX012283
VERSION AX012283.1 GI:9998344
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct

ORIGIN

AX012283
Sequence 45 from Patent WO9955856.
AX012283
synthetic construct
synthetic construct

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 45 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
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QY 1 BKS GCAUGGCUAAGGACCC 20
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Db 38 TTCGCATGGCTAAGGACCC 57

RESULT 3
AX012284
LOCUS          AX012284
DEFINITION    Sequence 46 from Patent WO9955856.
ACCESSION     AX012284
VERSION       AX012284.1 GI:9998345
KEYWORDS      .
SOURCE        synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 46 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source
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  /note="synthetic nucleic acid"
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Query Match      92.0%; Score 18.4; DB 6; Length 57;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKS GCAUGGCUAAGGACCC 20
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Db 38 CGGCATGGCTAAGGACCC 57

RESULT 4
AX012285
LOCUS          AX012285
DEFINITION    Sequence 47 from Patent WO9955856.
ACCESSION     AX012285
VERSION       AX012285.1 GI:9998346
KEYWORDS      .
SOURCE        synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 47 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 45 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
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Query Match      92.0%; Score 18.4; DB 6; Length 57;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKS GCAUGGCUAAGGACCC 20
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Db 38 TTCGCATGGCTAAGGACCC 57

RESULT 5
AX012286
LOCUS          AX012286
DEFINITION    Sequence 48 from Patent WO9955856.
ACCESSION     AX012286
VERSION       AX012286.1 GI:9998347
KEYWORDS      .
SOURCE        synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 48 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 75.0%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 BKS GCAUGGCUAAGGACCC 20
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Db 38 TTCGCATGGCTAAGGACCC 57

RESULT 6
AX012287
LOCUS          AX012287
DEFINITION    Sequence 49 from Patent WO9955856.
ACCESSION     AX012287
VERSION       AX012287.1 GI:9998348
KEYWORDS      .
SOURCE        synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE        Nucleic acid enzyme for rna cleavage
JOURNAL      Patent: WO 9955856-A 49 04-NOV-1999;
              ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
              PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 75.0%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 38 TTCGCATGGCTAAGGACCC 57
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RESULT 7
AX012288
LOCUS AX012288 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 50 from Patent WO9955856.
ACCESSION AX012288
VERSION AX012288.1 GI:9998349
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 50 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Location/Qualifiers
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ORIGIN
Query Match      92.0%; Score 18.4; DB 6; Length 57;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKS GCAUGGCUAAGGACCC 20
Db 38 TTCGCATGGCTAAGGACCC 57
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RESULT 8
AX012289
LOCUS AX012289 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 51 from Patent WO9955856.
ACCESSION AX012289
VERSION AX012289.1 GI:9998350
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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Best Local Similarity 75.0%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 38 TTCGCATGGCTAAGGACCC 57
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RESULT 9
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LOCUS AX012290 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO9955856.
ACCESSION AX012290
VERSION AX012290.1 GI:9998351
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 52 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 75.0%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 BKS GCAUGGCUAAGGACCC 20
Db 38 TTCGCATGGCTAAGGACCC 57
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RESULT 10
AX012292
LOCUS AX012292 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 54 from Patent WO9955856.
ACCESSION AX012292
VERSION AX012292.1 GI:9998353
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 54 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGC AUGGCUAAGGACCC 20
Db 1 GGCATGGCTAAGGACCC 18
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      :|||:|||||

RESULT 11
AC118386
LOCUS AC118386 236694 bp DNA linear HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-397N16, *** SEQUENCING IN PROGRESS

```

***, 3 unordered pieces.	COMMENT	On Nov 15, 2002 this sequence version replaced gi:23812823. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
AC118386		----- Genome Center
AC118386.4 GI:25013229		Center: Baylor College of Medicine
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.		Center code: BCM
Rattus norvegicus (Norway rat)		Web site: http://www.hgsc.bcm.tmc.edu/
Rattus norvegicus		Contact: hgsc-help@bcm.tmc.edu
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		----- Project Information
1 (bases 1 to 236694)		Center project name: GUEK
Muzny, D.Marie, Metzker, M.Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Kocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Loulseghe, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczkyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, E., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.		----- Summary Statistics
Direct Submission		Assembly program: Phrap; version 0.990329
2 (bases 1 to 236694)		Consensus quality: 175902 bases at least Q40
Worley, K.C.		Consensus quality: 179521 bases at least Q30
Direct Submission		Consensus quality: 181489 bases at least Q20
Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		Estimated insert size: 182948; sum-of-contigs estimation
3 (bases 1 to 236694)		Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
Rat Genome Sequencing Consortium.		-----
Direct Submission		* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
REFERENCE		* 1 217900: contig of 217900 bp in length
AUTHORS		* 217901 218000: gap of unknown length
TITLE		* 218001 234816: contig of 16816 bp in length
JOURNAL		* 234817 234916: gap of unknown length
		* 234917 236694: contig of 1778 bp in length.
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	Best Local Similarity	75.0%; Pred. No. 1.1e+02;

obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AL590988.

FEATURES

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Db 150188 GGGGCGATGCTCAGGGACCC 150169

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DEFINITION Homo sapiens chromosome 3 clone RP11-539L2, complete sequence.
ACCESSION AC092503 AC053519
VERSION AC092503.2 GI:18873863
KEYWORDS HTG.

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DEFINITION	Mus musculus chromosome 18 clone RP24-143K24 map 18, *** SEQUENCING					
IN PROGRESS ***						
ACCESSION	AC108403					
VERSION	AC108403.11 GI:50253677					
KEYWORDS	HTG; HTGS PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
REFERENCE	1 (bases 1 to 144393)					
AUTHORS	Birren,B., Nusbaum,C. and Lander,E.					

TITLE JOURNAL REFERENCE AUTHORS

Mus musculus chromosome 18, clone RP24-143K24
Unpublished
2 (bases 1 to 144393)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeAngelano, K., Dewar, K., Diaz, J., S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
Lander, E., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL REFERENCE AUTHORS

Submitted (27-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 144393)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V.,
Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J.,
Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
DeAngelano, K., Diaz, J., S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lander, E.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,
McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
Zimmer, A. and Zody, M.

TITLE JOURNAL COMMENT

Submitted (13-JUL-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2004 this sequence version replaced gi:45861136.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
----- Project Information
Center project name: L18687
Center clone name: 143_K_24

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as runs of N. The order of the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced

* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*

FEATURES
source

1 Location/Qualifiers
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Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGGACCC 20
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Db 84455 TGGCAAGGCTAAGGGACCC 84473

Search completed: March 15, 2005, 12:35:12
Job time : 397.807 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 11:20:37 ; Search time 110.965 Seconds
(without alignments)
1066.957 Million cell updates/sec

Title: US-09-699-667E-66
Perfect score: 20
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Scoring table: IDENTITY_NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4316768

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
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- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18.4	92.0	20	3	Aaz57640 Nucleotid
2	18.4	92.0	57	3	Aaz57636 Trans-act
3	18.4	92.0	57	3	Aaz57638 Trans-act
4	18.4	92.0	57	3	Aaz57637 Trans-act
5	15	75.0	29	12	Adl66390 Human Nkd
6	14.4	72.0	39	2	Aaq88793 Rat IL-2
7	14.2	71.0	30	3	Aaz31989 PCR prime
8	14	70.0	24	3	Aaa92220 Hsc70-PRL
9	14	70.0	24	3	Aaa92212 Hsc70-PYE
10	14	70.0	24	3	Aaa92216 Hsc70ATPA
11	13.8	69.0	27	2	Aav70405 Hepatitis
12	13.8	69.0	41	2	Aax78133 Hepatitis
13	13.8	69.0	45	13	Adt47042 Dengue vi
14	13.8	69.0	45	13	Adt48967 PCR prime
15	13.8	69.0	48	2	Aat30818 HDV riboz
16	13.8	69.0	48	2	Aav42395 Reverse P
17	13.8	69.0	48	2	Aav60155 Reverse P
18	13.8	69.0	48	2	Aav70715 Reverse p
19	13.8	69.0	48	3	Aaz92931 Hepatitis
20	13.8	69.0	48	3	Aaz92804 Hepatitis

C 21	13.8	69.0	48	6	AAL38811	Aal38811 Alphaviru
C 22	13.8	69.0	48	6	ABK46277	Abk46277 HDV antic
C 23	13.8	69.0	48	12	ADI30384	Adi30384 Hepatitis
C 24	13.8	69.0	48	12	ADO13943	Ado13943 Eukaryoti
C 25	13.8	69.0	55	13	ADR47041	Adr47041 Dengue vi
C 26	13.8	69.0	55	13	ADT48966	Adt48966 PCR prime
C 27	13.8	69.0	56	2	AAQ86203	Aaq86203 Sindbis/H
C 28	13.8	69.0	56	2	AAQ86174	Aaq86174 Primer HD
C 29	13.8	69.0	56	2	AAT30850	Aat30850 HDV forwa
C 30	13.8	69.0	56	2	AAV42425	Aav42425 Forward P
C 31	13.8	69.0	56	2	AAV60184	Aav60184 Forward P
C 32	13.8	69.0	56	2	AAV70745	Aav70745 Forward P
C 33	13.8	69.0	56	3	AAZ92969	Aaz92969 Hepatitis
C 34	13.8	69.0	56	3	AAZ92842	Aaz92842 Hepatitis
C 35	13.8	69.0	56	6	AAL38849	Aal38849 Alphaviru
C 36	13.8	69.0	56	6	ABK46315	Abk46315 Hepatitis
C 37	13.8	69.0	56	12	ADI30422	Adi30422 Hepatitis
C 38	13.8	69.0	56	12	ADO13981	Ado13981 Eukaryoti
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42	13.6	68.0	47	2	AAT63994	Aat63994 Human ren
43	13.6	68.0	47	2	AAX17282	Aax17282 Test sequ
44	13.6	68.0	47	6	ABK82773	Abk82773 DNA bindi
45	13.6	68.0	47	12	AD80312	Ad80312 Duplex ol
C	13.6	68.0	51	4	AAL30821	Aal30821 Human SNP

ALIGNMENTS

RESULT 1
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ID AAZ57640 standard; RNA; 20 BP.
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AC AAZ57640;
XX
DT 05-APR-2000 (first entry)
XX
DE Nucleotide sequence of bimolecular ribozyme RzB fragment.
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KW Bimolecular ribozyme; viral RNA cleavage; RzA fragment;
KW inherited disease; ss.
XX
OS Synthetic.
XX
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FT /note= "Forms double-stranded region with bases 37-30 of
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FT /note= "Forms double-stranded region with bases 6-1 of
FT sequence AAZ57639"

WO9955856-A2.

04-NOV-1999.

29-APR-1999; 99WO-CA0000391.

29-APR-1999; 98CA-02230203.

(UYSH) UNIV SHERBROOKE.

Perreault J, Ananvoranich S, Lafontaine D;

WPI; 2000-096791/08.

New construction of nucleic acid enzyme useful for biotechnological,
diagnostic and therapeutic applications.

```

XX
PS Example 5; Fig 4; 52pp; English.
CC This is the nucleotide sequence of bimolecular ribozyme R2B fragment.
CC relates to a nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed
CC to have a substrate binding portion with the following sequence 3'-UNNXXN
CC -5'. The substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The
CC binding portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3'
CC to the cleavage site of the substrate (cleavage site is represented by
CC *). At least one nucleotide is present 5' to the cleavage site of the
CC substrate sequence. The enzyme of the invention is used to cleave a
CC substrate nucleotide sequence at a specific cleavage site by mixing the
CC substrate with the enzyme. The enzyme is used to cleave viral RNA or RNA
CC causing for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
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SQ Sequence 20 BP; 4 A; 6 C; 8 G; 0 T; 2 U; 0 Other;
    Query Match          92.0%; Score 18.4; DB 3; Length 20;
    Best Local Similarity 85.0%; Pred. No. 6.9;
    Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGCGCAUGGCUAAGGACCC 20

RESULT 2
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ID AAZ57636 standard; RNA; 57 BP.
AC AAZ57636;
XX
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence.
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzP1.1; ss.
OS Synthetic.
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FT misc_binding 20..25
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PF 29-APR-1999; 99WO-CA000391.
XX
PR 29-APR-1998; 98CA-02230203.
XX
PA (UYSH ) UNIV SHERBROOKE.
XX
PI Perreault J, Ananvoranich S, Lafontaine D;
XX
DR WPI; 2000-096791/08.
XX
PT New construction of nucleic acid enzyme useful for biotechnological,

```

```

PT diagnostic and therapeutic applications.
XX
PS Example 1; Fig 1A; 52pp; English.
XX
CC This is the nucleotide sequence of ribozyme deltaRzP1.1. This ribozyme
CC cleaves substrate SP1.1 (see AAZ57641). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzP1.1) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
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SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
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    Best Local Similarity 85.0%; Pred. No. 7.7;
    Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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AC AAZ57638;
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DT 15-SEP-2003 (revised)
DT 05-APR-2000 (first entry)
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DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; ss.
XX
OS Hepatitis D virus.
XX
FH Key Location/Qualifiers
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   /tag= a
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FT stem_loop 7..19
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FT stem_loop 30..45
   /bound_moiety= "SP1.1 substrate bases (AAZ57641) 5-11"
FT misc_binding 52..57
   /tag= d
FT misc_binding 52..57
   /tag= e
   /note= "Forms a double stranded region with bases 6-1"
XX
PN WO9955856-A2.
XX
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-CA000391.
XX
PR 29-APR-1998; 98CA-02230203.
XX
PA (UYSH ) UNIV SHERBROOKE.
XX
PI Perreault J, Ananvoranich S, Lafontaine D;
XX
DR WPI; 2000-096791/08.
XX

```


XX PT New construction of nucleic acid enzyme useful for biotechnological,
 XX PT diagnostic and therapeutic applications.
 XX PS Example 1; Fig 2; 52pp; English.
 XX CC This is the nucleotide sequence of a trans-acting antigenomic delta
 CC ribozyme of the invention. This ribozyme cleaves substrate SPL1.1 (see
 CC AAZ57641). The invention relates to a nucleic acid enzyme (e.g.
 CC deltaRzPl.1) that is constructed to have a substrate binding portion with
 CC the following sequence 3'-UNNXXN-5'. The substrate of the enzyme has the
 CC sequence 5'-H*GNNHNN-3'. The binding portion of the enzyme (ribozyme)
 CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate
 CC (cleavage site is represented by *). At least one nucleotide is present
 CC 5' to the cleavage site of the substrate sequence. The enzyme of the
 CC invention is used to cleave a substrate nucleotide sequence at a specific
 CC cleavage site by mixing the substrate with the enzyme. The enzyme is used
 CC to cleave viral RNA or RNA causing for example an inherited disease. The
 CC enzymes also have other therapeutic, biotechnological and diagnostic
 CC applications. (Updated on 15-SEP-2003 to standardise OS field)
 XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
 Query Match 92.0%; Score 18.4; DB 3; Length 57;
 Best Local Similarity 85.0%; Pred. No. 7.7;
 Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 BKSGCAUGGCUAAGGGACCC 20
 Db 38 CGGCAUGGCUAAGGGACCC 57
 RESULT 4
 AAZ57637
 ID AAZ57637 standard; RNA; 57 BP.
 AC AAZ57637;
 DT 05-APR-2000 (first entry)
 DE Trans-acting antigenomic delta ribozyme, deltaRzPl.2 nucleotide sequence.
 XX KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
 KW inherited disease; deltaRzPl.2; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT misc_binding 1..6
 FT /*tag= a
 FT /note= "Forms double stranded region with bases 52-57"
 FT 7..19
 FT /*tag= b
 FT 20..25
 FT /*tag= c
 FT /bound_moiety= "SPL1.2 substrate bases (AAZ57634) 6-11"
 FT 30..45
 FT /*tag= d
 FT 52..57
 FT /*tag= e
 FT /note= "Forms a double stranded region with bases 6-11"
 FT WO9955856-A2.
 XX PN 04-NOV-1999.
 XX PD 29-APR-1999; 99WO-CA000391.
 XX PR 29-APR-1999; 98CA-02230203.
 XX PA (UYSH) UNIV SHERBROOKE.
 XX PI Perreault J, Ananvoranich S, Lafontaine D;

XX WPI; 2000-096791/08.
 XX New construction of nucleic acid enzyme useful for biotechnological,
 XX PT diagnostic and therapeutic applications.
 XX PS Example 1; Page; 52pp; English.
 XX CC This is the nucleotide sequence of ribozyme deltaRzPl.2. This ribozyme
 CC cleaves substrate SPL1.2 (see AAZ57634). The invention relates to a
 CC nucleic acid enzyme (e.g. deltaRzPl.2) that is constructed to have a
 CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
 CC substrate of the enzyme has the sequence 5'-H*GNNHNN-3'. The binding
 CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
 CC cleavage site of the substrate (cleavage site is represented by *). At
 CC least one nucleotide is present 5' to the cleavage site of the substrate
 CC sequence. The enzyme of the invention is used to cleave a substrate
 CC nucleotide sequence at a specific cleavage site by mixing the substrate
 CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
 CC for example an inherited disease. The enzymes also have other
 CC therapeutic, biotechnological and diagnostic applications. Note: This
 CC sequence is not shown in the specification, but has been derived from the
 CC deltaRzPl.1 sequence (AAZ57636) shown in figure 1
 XX SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
 Query Match 92.0%; Score 18.4; DB 3; Length 57;
 Best Local Similarity 85.0%; Pred. No. 7.7;
 Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 BKSGCAUGGCUAAGGGACCC 20
 Db 38 UUGCGAUGGCUAAGGGACCC 57
 RESULT 5
 ADL66390
 ID ADL66390 standard; DNA; 29 BP.
 XX AC ADL66390;
 XX DT 03-JUN-2004 (first entry)
 XX DE Human Nkd1 (CGX7) RT-PCR primer, SEQ ID NO:46.
 XX KW Human; colon and gastric cancer-associated; CGX protein;
 KW colorectal cancer; colon cancer; gastric cancer; antisense therapy;
 KW gene silencing; drug screening; detection; diagnosis; predisposition;
 KW cytostatic; vaccine; CGX7; Nkd1; reverse transcription-PCR; RT-PCR;
 KW primer; ss.
 XX OS Homo sapiens.
 XX PN WO2004021010-A2.
 XX PD 11-MAR-2004.
 XX PF 19-AUG-2003; 2003WO-JP010436.
 XX PR 30-AUG-2002; 2002US-0407338P.
 XX PA (ONCO-) ONCOTHERAPY SCI INC.
 XX PA (UYTY) UNIV TOKYO.
 XX PI Nakamura Y, Furukawa Y;
 XX DR WPI; 2004-239234/22.
 XX New CGX polypeptides and polynucleotides, useful in diagnosing, treating
 XX and/or preventing colon and gastric cancers.
 XX Example 1; SEQ ID NO 46; 228pp; English.

CC The invention relates to human colon and gastric cancer-associated (CGX)
 CC proteins and their encoding nucleic acids which are differentially
 CC expressed in colorectal or gastric cancer. 7 of the 8 CGX genes
 CC identified showed increased expression in colorectal cancers while the
 CC eighth CGX protein, LAPTM4beta (CGX8), showed increased expression in
 CC gastric cancer. Of the 7 colon cancer-associated genes, 2 (Ly6E (CGX6)
 CC and Nkd1 (CGX7)) were known but had not previously been associated with
 CC colon cancer, and 5 were novel. The novel colon cancer-associated genes
 CC are: ABHCL1 (CGX1, ADL66345); C20orf20 (CGX3, ADL66347); CCPUCC1 (CGX5,
 CC ADL66349); LEMD1S and LEMD1L (both designated CGX4, ADL66351 and
 CC ADL66353); and NFXL1 (CGX2, ADL66355). The proteins encoded by these
 CC novel genes are given in ADL66346, ADL66348, ADL66350, ADL66352, ADL66354
 CC and ADL66356. The invention also relates to vectors and host cells
 CC comprising a CGX1-5 nucleic acid; methods for the recombinant production
 CC of CGX1-5 antibodies specific for CGX1-5; antisense polynucleotides or
 CC small interfering RNA (siRNA) targeted to the CGX1-5 or CGX8 genes;
 CC methods of treating or preventing colon or gastric cancer; methods of
 CC screening for compounds for treating or preventing colon or gastric
 CC cancer; DNA arrays comprising CGX1-7 or CGX8 probes; kits for detecting
 CC CGX1-7 or CGX8 polynucleotides or polypeptides; colon cancer reference
 CC expression profiles comprising a pattern of gene expression of two or
 CC more genes selected from CGX1-7; a method for inducing antitumour
 CC immunity; and compositions for the treatment or prevention of colon or
 CC gastric cancer comprising a pharmaceutical amount of a CGX polypeptide or
 CC fragment thereof, an anti-CGX antibody, an antisense polynucleotide, an
 CC siRNA, or a compound identified by screening. The polypeptides,
 CC polynucleotides, compounds, kits or composition are useful in diagnosing
 CC colon and gastric cancer or a predisposition to developing colon or
 CC gastric cancer and in treating or preventing colon and gastric cancer.
 CC The present sequence represents a reverse transcription-PCR (RT-PCR)
 CC primer used in an example of the invention.

XX SQ Sequence 29 BP; 4 A; 9 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 12; Length 29;
 Best Local Similarity 68.4%; Pred. No. 4.6e+02;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGGACCC 20
 :|||:||||:|||||
 Db 9 GCGCATGGCTTAGGGACGC 27

RESULT 6
 AAQ88793
 ID AAQ88793 standard; DNA; 39 BP.
 XX
 AC AAQ88793;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-AUG-1995 (first entry)
 XX
 DE Rat IL-2 upstream PCR primer # 1.
 XX
 KW Interleukin-2; IL-2; PCR primer; plasmid pMV261; ss.
 XX
 OS Synthetic.
 XX
 FN WO9503418-A2.
 XX
 PD 02-FEB-1995.
 XX
 PF 22-JUL-1994; 94WO-US008215.
 XX
 PR 22-JUL-1993; 93US-00096027.
 XX
 PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Odonnell MA, Duda RB, Dewolf WC, Aldovini A, Young RA, Murray PJ;
 XX WPI; 1995-075244/10.
 XX

PT New recombinant mycobacteria and plasmids - express cytokine(s),
 PT lymphokine(s), enzymes, etc extracellularly, for use as BCG vaccines and
 PT in cancer therapy.
 XX
 PS Example; Page 16; 46pp; English.

XX A set of E.coli-BCG shuttle plasmids were constructed to permit prodn. of
 CC IL-2. Three sets of paired oligo primers were utilised in the PCR with
 CC appropriate templates to produce insert DNAs with ends suitable for
 CC cloning in the plasmid pMV261. The oligo primers were AAQ88793-088798,
 CC primer nos. 1-6 respectively. The rat and mouse IL-2 upstream primers no.
 CC 1 and no. 3 respectively were constructed to anneal with the IL-2 coding
 CC regions starting at codon 21 thereby excluding their native signal
 CC peptide regions. The BCG alpha antigen downstream primer no. 4 terminated
 CC at the sequence encoding the putative protease cleavage site ala-gly-ala
 CC (Terasake et al., FEMS Lett. 58:273-276 1989. (Updated on 25-MAR-2003 to
 CC correct FN field.)
 XX

SQ Sequence 39 BP; 9 A; 15 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 2; Length 39;
 Best Local Similarity 77.8%; Pred. No. 9.8e+02;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SGCAUGGCUAAGGGACCC 20
 :|||:||||:|||||
 Db 1 GCGATGGCCAAGGGATCC 18

RESULT 7
 AAZ31989
 ID AAZ31989 standard; DNA; 30 BP.
 XX
 AC AAZ31989;

DT 28-JAN-2000 (first entry)

DE PCR primer for glucagon-like peptide-1 mutein coding sequence.

XX Glucagon-like peptide-1; GLP-1; mutein; type II diabetes mellitus;
 KW insulinotropic peptide; non-insulin dependent diabetes mellitus; obesity;
 KW therapy; PCR primer; ss.
 XX

OS Synthetic.

FN WO9953064-A2.

XX 21-OCT-1999.

PF 13-APR-1999; 99WO-IB000651.

PR 13-APR-1998; 98US-0081562P.

PR 12-APR-1999; 99US-00081562.

XX (MODE-) MODEX THERAPEUTICS SA.

XX Thorens B;

DR WPI; 2000-013103/01.

PT Treating type II diabetes mellitus and obesity using glucagon like
 PT peptide.
 XX

PS Example 4; Page 19; 33pp; English.

XX This sequence represents PCR primer used to isolate DNA encoding a
 CC glucagon-like peptide-1 (GLP-1) mutein. The invention relates to a method
 CC for treating type II diabetes mellitus, by administering a GLP-1 or a GLP
 CC -1 mutein, particularly the mutein GLP-1-Gly8. The GLP-1 mutein is an
 CC insulinotropic peptide. The method is used to treat type II diabetes (non
 CC -insulin dependent diabetes mellitus) and obesity

XX SQ Sequence 30 BP; 8 A; 5 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 30;
 Best Local Similarity 68.4%; Pred. No. 1.2e+03;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGACC 19
 DB 12 TTCGATGCTAAGGACC 30

RESULT 8
 AAA92220
 ID AAA92220 standard; DNA; 24 BP.
 XX
 AC AAA92220;
 XX
 DT 05-JAN-2001 (first entry)
 XX
 DE Hsc70-PYE oligonucleotide primer SEQ ID NO:70.
 XX
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
 KW immune response; infectious disease; malaria; cytotoxic T cell;
 KW cytoskeletal; immunostimulant; cellular immune response inducer;
 KW protozoacide; leukaemia; cancer; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200049041-A1.
 XX
 PD 24-AUG-2000.
 XX
 PF 18-FEB-2000; 2000WO-JP000941.
 XX
 PR 19-FEB-1999; 99JP-00041535.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX
 PI Shinbara N, Udono H, Yui K;
 XX
 DR WPI; 2000-543748/49.
 XX
 PT Fused protein capable of inducing cellular immune response, useful as
 PT active ingredient for drug compositions in preventing and/or treating
 PT infectious diseases such as malaria or cancer.
 XX
 PS Example 1; Page 17; 72pp; Japanese.
 XX
 CC The present invention describes a fused protein (I) prepared from a
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat
 CC shock protein. Also described are: (1) a drug composition containing (I)
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
 CC containing the DNA of (2); and (4) a transformant which can retain the
 CC expression vector of (3). (I) has cytostatic, immunostimulant and
 CC protozoacide activities, and can be used as a cellular immune response
 CC inducer. The protein is useful as an active ingredient for drug
 CC compositions in preventing and/or treating infectious diseases such as
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
 CC The present sequence represents a primer which is used in an example from
 CC the present invention
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 3; Length 24;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGACC 19
 DB 6 TCCCATGCTAAGGACC 23

RESULT 9
 AAA92216
 ID AAA92216 standard; DNA; 24 BP.
 XX
 AC AAA92216;
 XX
 DT 05-JAN-2001 (first entry)
 XX
 DE Hsc70ATPase domain-PYE oligonucleotide primer SEQ ID NO:66.
 XX
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
 KW immune response; infectious disease; malaria; cytotoxic T cell;

AAA92212
 ID AAA92212 standard; DNA; 24 BP.
 XX
 AC AAA92212;
 XX
 DT 05-JAN-2001 (first entry)
 XX
 DE Hsc70-PYE oligonucleotide primer SEQ ID NO:62.
 XX
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
 KW immune response; infectious disease; malaria; cytotoxic T cell;
 KW cytoskeletal; immunostimulant; cellular immune response inducer;
 KW protozoacide; leukaemia; cancer; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200049041-A1.
 XX
 PD 24-AUG-2000.
 XX
 PF 18-FEB-2000; 2000WO-JP000941.
 XX
 PR 19-FEB-1999; 99JP-00041535.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX
 PI Shinbara N, Udono H, Yui K;
 XX
 DR WPI; 2000-543748/49.
 XX
 PT Fused protein capable of inducing cellular immune response, useful as
 PT active ingredient for drug compositions in preventing and/or treating
 PT infectious diseases such as malaria or cancer.
 XX
 PS Example 1; Page 16; 72pp; Japanese.
 XX
 CC The present invention describes a fused protein (I) prepared from a
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat
 CC shock protein. Also described are: (1) a drug composition containing (I)
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
 CC containing the DNA of (2); and (4) a transformant which can retain the
 CC expression vector of (3). (I) has cytostatic, immunostimulant and
 CC protozoacide activities, and can be used as a cellular immune response
 CC inducer. The protein is useful as an active ingredient for drug
 CC compositions in preventing and/or treating infectious diseases such as
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
 CC The present sequence represents a primer which is used in an example from
 CC the present invention
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 3; Length 24;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 KSGCAUGGCUAAGGACC 19
 DB 6 TCCCATGCTAAGGACC 23

RESULT 10
 AAA92216
 ID AAA92216 standard; DNA; 24 BP.
 XX
 AC AAA92216;
 XX
 DT 05-JAN-2001 (first entry)
 XX
 DE Hsc70ATPase domain-PYE oligonucleotide primer SEQ ID NO:66.
 XX
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
 KW immune response; infectious disease; malaria; cytotoxic T cell;

KW cytostatic; immunostimulant; cellular immune response inducer;
 KW protozoacide; leukaemia; cancer; primer; ss.
 XX Synthetic.
 OS

XX WO200049041-A1.
 PN

XX 24-AUG-2000.
 PD

XX 18-FEB-2000; 2000WO-JP000941.
 PF

XX 19-FEB-1999; 99JP-00041535.
 PR

XX (SUME) SUMITOMO ELECTRIC IND CO.
 PA

XX Shinbara N, Udono H, Yui K;
 PI

XX WPI; 2000-543748/49.
 DR

XX Fused protein capable of inducing cellular immune response, useful as
 PT active ingredient for drug compositions in preventing and/or treating
 PT infectious diseases such as malaria or cancer.
 XX

XX Example 1; Page 16; 72pp; Japanese.
 PS

CC The present invention describes a fused protein (I) prepared from a
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat
 CC shock protein. Also described are: (1) a drug composition containing (I)
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
 CC containing the DNA of (2); and (4) a transformant which can retain the
 CC expression vector of (3). (I) has cytostatic, immunostimulant and
 CC protozoacide activities, and can be used as a cellular immune response
 CC inducer. The protein is useful as an active ingredient for drug
 CC compositions in preventing and/or treating infectious diseases such as
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
 CC The present sequence represents a primer which is used in an example from
 CC the present invention
 XX

SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 3; Length 24;

Best Local Similarity 66.7%; Pred. No. 1.5e+03;

Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 KSGCAUGGCUAAGGGACC 19

DB 6 TCCCATGCTAAGGGACC 23

RESULT 11

AAV70405/C

ID AAV70405 standard; DNA; 27 BP.

XX AAV70405;

AC AAV70405;

DT 01-MAR-1999 (first entry)

XX Hepatitis delta virus anti-genome ribozyme primer.

DE HPIV-3; human parainfluenza virus type 3; vaccine; ribozyme; PCR; primer;

XX 86.

KW Synthetic.

OS Hepatitis D virus.

XX WO9850405-A1.

PN 12-NOV-1998.

PD 06-MAY-1998; 98WO-US009270.

XX 07-MAY-1997; 97US-0045805P.

PR

XX (CLEV-) CLEVELAND CLINIC FOUND.
 PA

XX Banerjee AK, Hoffman MA;
 PI

XX WPI; 1998-610318/51.
 DR

XX New human parainfluenza virus (HPIV) clone, and - methods of clone
 PT production and introduction of site-specific mutations.
 PT

XX Example 1; 7pp; 54pp; English.
 PS

XX This primer encodes the 3' end of a hepatitis delta virus antigenomic
 CC ribozyme and a BglII site. It was used with a second primer (see
 CC AAV70404) which contains a sequence from the 3' untranslated region of
 CC human parainfluenza virus type 3 (HPIV-3) L mRNA, through to the trailer
 CC portion of the HPIV-3 genome (see AAV70404), and which also primes
 CC synthesis of the ribozyme, in the PCR amplification of the ribozyme. The
 CC product was used in the construction of a full-length cDNA clone of HPIV-
 CC 3. The invention relates to a system for generating recombinant HPIV such
 CC as a clone comprising a nucleotide sequence that encodes a full-length,
 CC positive sense, anti-genome of HPIV. The invention also relates to a
 CC method of preparing recombinant HPIV-3 having site-directed mutations.
 CC Production of recombinant HPIV clones enables analysis of HPIV
 CC transcription and replication in a cell-free system. A system which
 CC permits production of recombinant HPIV that is genetically engineered to
 CC contain site-specific mutations is useful for identifying attenuating
 CC genotypes useful for developing live vaccines
 XX

SQ Sequence 27 BP; 4 A; 10 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 27;

Best Local Similarity 64.7%; Pred. No. 2e+03;

Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 BKSGCAUGGCUAAGGGA 17

DB 26 CTCGGATGGCTAAGGGA 10

RESULT 12

AAV78133

ID AAV78133 standard; DNA; 41 BP.

XX AAV78133;

DT 20-AUG-1999 (first entry)

XX Hepatitis D virus ribozyme fragment 2.

KW Alphavirus; replicon; expression vector; heterologous splice site;
 KW RNA splicing; viral RNA replication; antigen; vaccination; therapy;
 KW ribozyme; ss.

OS Hepatitis D virus.

XX WO9925859-A1.

PN 27-MAY-1999.

XX 13-NOV-1998; 98WO-CA001065.

XX 14-NOV-1997; 97US-0065793P.

XX (CONN-) CONNAUGHT LAB LTD.

XX Parrington M;

XX WPI; 1999-385140/32.

DR

XX New vector (EV) used to express an antigen for vaccination, e.g. against

PT human immune deficiency virus.

XX

PS Disclosure; Fig 9; 60pp; English.

XX This invention describes the construction of a novel expression vector

CC (EV) containing an alphavirus replicon having a heterologous splice site.

CC The expression vector contains (i) a DNA molecule (I) complementary to at

CC least part of an alphavirus RNA genome, and (ii) inserted into a region

CC of (I) that is not essential for its replication, a heterologous DNA

CC (II), under control of a promoter. (I) includes at least one heterologous

CC splice site (HSS) to prevent aberrant RNA splicing of the alphavirus and

CC is the complement of the complete alphavirus genomic region essential for

CC replication of viral RNA. The expression vector is used to express (II)

CC in humans or animals, e.g. to express an antigen for vaccination (against

CC human immune deficiency virus) or to produce a therapeutically active

CC protein or peptide. Introducing an HSS: (1) makes it more likely that any

CC splicing will occur at this site, rather than at a cryptic splice site;

CC (2) restores function of the alphavirus when eliminated, and (3) may

CC improve transport of RNA from the nucleus

XX Sequence 41 BP; 11 A; 10 C; 15 G; 5 T; 0 U; 0 Other;

SQ

Query Match 69.0%; Score 13.8; DB 2; Length 41;

Best Local Similarity 64.7%; Pred. No. 2.1e+03;

Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 BKSGCAUGGCUAAGGGA 17

DB 23 CTCGGATGCTAAGGGA 39

RESULT 13

ID ADR47042

XX ADR47042 standard; DNA; 45 BP.

AC ADR47042;

XX

DT 18-NOV-2004 (first entry)

XX

DE Dengue virus vaccine oligonucleotide #17.

XX

XX ss; cytosstatic; virucide; dengue virus; recombinant replicon; deletion;

KW prem protein; C protein; NS1 protein signal; vaccine; cervical cancer;

KW viral disease; antigen; dendritic cell; immune response;

KW human papillomavirus.

XX

OS Unidentified.

XX

PN WO200407274-A1.

XX

PD 26-AUG-2004.

XX

PF 30-JAN-2004; 2004WO-CN000089.

XX

PR 30-JAN-2003; 2003CN-00115272.

PR 30-JAN-2003; 2003CN-00115273.

XX

PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.

PA (TENG-) TENGGEN BIOMEDICAL CO.

PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

XX

PI Pang X;

XX

DR WPI; 2004-625870/60.

XX

PT Virus-like particle vaccines containing dengue virus recombinant replicon

PT as core for carrier, applicable in preventives or/and remedies for tumors

PT like cervical cancer and viral diseases.

XX

PS Example 4; SEQ ID NO 39; 38pp; Chinese.

XX

XX A dengue virus recombinant replicon has a deletion of the complete coding

CC sequence for prem protein of dengue virus and also includes elements of

CC e.g. the non-coding region in the whole of the 5'-end, the coding region

CC of the front 20 amino acids in the C protein, and the coding region of

CC

CC NS1 protein signal; coding regions of all non-structural proteins. The

CC obtained vaccines are useful in producing preventives or/and remedies for

CC cancer like cervical cancer and viral diseases. Such vaccines can

CC efficiently express antigen in infected cells, which is because dengue

CC virus can infect dendritic cells, and can effectively present antigen to

CC provide immunity effect. Different types of dengue virus can be used to

CC repeatedly produce efficient immune response thereby strengthening the

CC body's immune system against the pathogen that contains such antigen.

CC Human papillomavirus (HPV) vaccines were prepared by using a gene-

CC expressing system using of the full-length dengue virus cDNA clone

CC (pRS/FLD2). The recombinant virus vectors were transfected into baby

CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell

CC lines. This sequence corresponds to an oligonucleotide used in the

CC recombinant replicon of the invention.

XX

SQ Sequence 45 BP; 16 A; 8 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 13; Length 45;

Best Local Similarity 64.7%; Pred. No. 2.1e+03;

Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 BKSGCAUGGCUAAGGGA 17

DB 4 CTCGGATGCTAAGGGA 20

RESULT 14

ID ADR48967

XX ADR48967 standard; DNA; 45 BP.

AC ADR48967;

XX

DT 16-DEC-2004 (first entry)

XX

DE PCR primer 5'pA, seq id 31.

XX

KW Virucide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;

KW PCR; primer; ss.

XX

OS Unidentified.

XX

PN WO2004082712-A1.

XX

PD 30-SEP-2004.

XX

PF 19-MAR-2004; 2004WO-CN000232.

XX

PR 20-MAR-2003; 2003CN-00115912.

XX

PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.

PA (TENG-) TENGGEN BIOMEDICAL CO.

PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

XX

PI Pang X;

XX

DR WPI; 2004-699719/68.

XX

PT Bivalent vaccines for preventing and treating Japanese (B) encephalitis

PT and hepatitis B produced by recombinant technique using encephalitis B

PT virus as vector to express antigen gene of hepatitis B.

XX

PS Example 8; SEQ ID NO 31; 33pp; Chinese.

XX

CC The invention relates to a recombinant Japanese encephalitis B virus

CC constructed from encephalitis B virus and a recombinant genome, where the

CC genome is inserted with an exogenous nucleotide sequence for

CC recombination and capable of retaining its self-replication function. The

CC virus is useful in producing the bivalent vaccines for preventing and

CC treating Japanese (B) encephalitis and hepatitis B. Such vaccines are

CC producible at low cost and have high immunoefficiency, in which the

CC recombinant virus can efficiently express the antigen of hepatitis B

CC virus with the safety and immunogenicity of attenuated encephalitis B

CC virus vaccines. The current sequence represents a PCR primer used in an

CC example from the invention.

XX Sequence 45 BP; 16 A; 8 C; 13 G; 8 T; 0 U; 0 Other;

SQ Query Match 69.0%; Score 13.8; DB 13; Length 45;

Best Local Similarity 64.7%; Pred. No. 2.1e+03;

Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 BKSGCAUGGCUAAGGGA 17

DB 4 CTCGGATGGCTAAGGGA 20

RESULT 15

AAT30818/c

ID AAT30818 standard; DNA; 48 BP.

XX AC AAT30818;

XX 12-SEP-1996 (first entry)

DE HDV ribozyme primer SHDV84R.

XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;

KW polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;

KW hepatitis delta virus; ss.

XX OS Synthetic.

XX PN WO9617072-A2.

XX PD 06-JUN-1996.

XX PF 30-NOV-1995; 95WO-US015490.

XX PR 30-NOV-1994; 94US-00348472.

PR 18-JAN-1995; 95US-00376184.

PR 15-MAR-1995; 95US-00405827.

XX PA (CHIR) CHIRON VIAGENE INC.

XX PI Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;

XX PI Belli BA;

XX DR WPI; 1996-277785/28.

XX PT New recombinant alpha-virus vectors - used to develop prods and methods

PT for use in gene therapy and in the prodn. of vaccines.

XX PS Example 3; Page 85; 256pp; English.

XX CC Primer SHDV84R (AAT30818) contains a buffer sequence allowing enzyme
CC digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme
CC sequence. It was used with nested primer HDV17-68 (AAT30817) and forward
CC primer SHDV1F (AAT30816) to generate an HDV ribozyme. This antigenomic
CC ribozyme can be placed between the polyA tract at the 3' end of a Sindbis
CC virus-based eukaryotic layered vector initiation system, ELVIS, and the
CC transcription terminal signals to produce alphavirus expression vectors
CC useful in methods of gene therapy and for vaccine prodn

XX SQ Sequence 48 BP; 7 A; 17 C; 10 G; 14 T; 0 U; 0 Other;

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Best Local Similarity 64.7%; Pred. No. 2.1e+03;

Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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DB 29 CTCGGATGGCTAAGGGA 13

Search completed: March 15, 2005, 16:13:07

Job time : 111.965 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 12:35:18 ; Search time 394.386 Seconds
(without alignments)
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Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1981570

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_in.*
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5: gb_ov.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	18.4	92.0	57	6	AX012283	AX012283 Sequence
3	18.4	92.0	57	6	AX012284	AX012284 Sequence
4	18.4	92.0	57	6	AX012285	AX012285 Sequence
5	18.4	92.0	57	6	AX012286	AX012286 Sequence
6	18.4	92.0	57	6	AX012287	AX012287 Sequence
7	18.4	92.0	57	6	AX012288	AX012288 Sequence
8	18.4	92.0	57	6	AX012289	AX012289 Sequence
9	18.4	92.0	57	6	AX012290	AX012290 Sequence
10	17.6	88.0	18	6	AX012292	AX012292 Sequence
11	15	75.0	29	6	CQ786869	CQ786869 Sequence
12	14.4	72.0	39	6	AR015975	AR015975 Sequence
13	14.4	72.0	39	6	AR050904	AR050904 Sequence
14	14.4	72.0	39	6	I33404	I33404 Sequence 4
15	13.8	69.0	27	6	BD191969	BD191969 Infectiou
16	13.8	69.0	48	6	AR021008	AR021008 Sequence
17	13.8	69.0	48	6	AR043423	AR043423 Sequence
18	13.8	69.0	48	6	AR062338	AR062338 Sequence
19	13.8	69.0	48	6	AR183797	AR183797 Sequence

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C 24	13.8	69.0	56	6	AR183835	AR183835 Sequence
C 25	13.8	69.0	56	6	AR368218	AR368218 Sequence
C 26	13.6	68.0	35	6	AR063795	AR063795 Sequence
C 27	13.6	68.0	35	6	I30158	I30158 Sequence 80
C 28	13.6	68.0	43	6	AR063796	AR063796 Sequence
C 29	13.6	68.0	43	6	I30159	I30159 Sequence 81
C 30	13.6	68.0	47	6	AR032670	AR032670 Sequence
C 31	13.6	68.0	47	6	I29410	I29410 Sequence 28
C 32	13.6	68.0	47	6	I91084	I91084 Sequence 28
C 33	13.6	68.0	47	6	AR209334	AR209334 Sequence
C 34	13.6	68.0	51	6	CQ005389	CQ005389 Sequence
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C 39	13.4	67.0	20	6	AR309456	AR309456 Sequence
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C 43	13.4	67.0	25	6	AX545652	AX545652 Sequence
C 44	13.4	67.0	25	6	AX545653	AX545653 Sequence
C 45	13.4	67.0	25	6	AX545654	AX545654 Sequence

ALIGNMENTS

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LOCUS AX012282 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 44 from Patent WO9955856.
ACCESSION AX012282
VERSION AX012282.1 GI:9998343
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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DEFINITION Sequence 45 from Patent WO9955856.
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VERSION AX012283.1 GI:9998344
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct

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REFERENCE
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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LOCUS AX012284 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9955856.
ACCESSION AX012284
VERSION AX012284.1 GI:9998345
KEYWORDS
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other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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LOCUS AX012285 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 47 from Patent WO9955856.
ACCESSION AX012285
VERSION AX012285.1 GI:9998346
KEYWORDS
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ORGANISM
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 45 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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DEFINITION Sequence 48 from Patent WO9955856.
ACCESSION AX012286
VERSION AX012286.1 GI:9998347
KEYWORDS
SOURCE
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synthetic construct
other sequences; artificial sequences.
REFERENCE
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AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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LOCUS AX012287 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 49 from Patent WO9955856.
ACCESSION AX012287
VERSION AX012287.1 GI:9998348
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 49 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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DEFINITION Sequence 50 from Patent WO955856.
ACCESSION AX012288
VERSION AX012288.1 GI:9998349
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 955856-A 50 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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DEFINITION Sequence 51 from Patent WO955856.
ACCESSION AX012289
VERSION AX012289.1 GI:9998350
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 955856-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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LOCUS AX012290 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 52 from Patent WO955856.
ACCESSION AX012290
VERSION AX012290.1 GI:9998351
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 955856-A 52 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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DEFINITION Sequence 54 from Patent WO955856.
ACCESSION AX012292
VERSION AX012292.1 GI:9998353
KEYWORDS
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ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 955856-A 54 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
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